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<120> EXTENDED CDNAS FOR SECRETED PROTEINS

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<140> 09/191,997
<141> 1998-11-13

<150> 60/066,677
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gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc     113
                                Met Lys Lys Val Leu Leu Leu Ile
                                        -15                 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag     161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                -5                  1               5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr     209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
        10                  15                  20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att     257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
    25                  30                  35
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata     305
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Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
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score 8.2
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Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

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actcctttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc 60
ctgatgccga gttccgtctc tcgcgtcttt tcctggtccc aggcaaagcg gasgnagatc 120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggtctaatt aattcctctg 180
gtttgttgaa gcagttacca agaatcttca accctttccc acaaaagcta attgagtaca 240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg 300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt 357
Met Trp Trp Phe
-20

cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
-15 -10 -5

gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
1 5 10 15

gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa 501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
20 25 30

aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa 549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
35 40 45

aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaaa 602
Lys

ctcttcaraa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt 662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg 722
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw 782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa 822

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<221> SIGNAL
<222> 1..21
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score 5.5
seq SFLPSALVIWTSA/AF
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Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val

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1               5                   10                  15
Ile Trp Thr Ser Ala
            20

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cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatattcc aggcctacct    120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg    180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg      229
     Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
              -35                 -30                 -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
        -20                 -15                 -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
    -5                  1               5                   10
cct gac aac taaatatcct tatccaaatc aataaarwra raatcctccc              374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaa a                                   405

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<223> Von Heijne matrix
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      seq LSYASSALSPCLT/AP
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Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1               5                   10                  15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
            20                  25                  30
Ser Pro Cys Leu Thr
        35

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attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg 120
cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag 180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt 231
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
-15 -10 -5
gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt 279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
1 5 10
gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg 327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
15 20 25
gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat 375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
30 35 40 45
tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc 424
Ser Ser Ala
atatttaaat tggaaaagtc aaattgasca ttattaaata aagcttgttt aatatgtctc 484
aaacaaaaaa aa 496

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score 5.5
seq ILSTVTALTFAXA/LD
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<221> UNSURE
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1 5 10 15

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Met Glu Arg
-15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
-10 -5 1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
5 10 15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac 201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20 25 30 35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta 249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
40 45 50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac 297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
55 60 65
atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc 345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
70 75 80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag 393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
85 90 95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg 441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100 105 110 115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc 489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
120 125 130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga 534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
135 140 145
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taaactctca tgcccccaaa aaaaaaaaa 623

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1 5 10 15

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                                                    -10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat       100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
        -5                  1               5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca       148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10                  15                  20                  25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct       196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
                30                  35                  40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat       244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
            45                  50                  55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt       292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
        60                  65                  70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca       340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
    75                  80                  85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat       388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
90                  95                  100                 105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc       436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
                110                 115                 120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt       484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
            125                 130                 135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg       532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
        140                 145                 150
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa       580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
    155                 160                 165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat       628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
170                 175                 180                 185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag       676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
                190                 195                 200
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcctcaaraa          727
Asp Glu Arg Leu Thr Pro Leu
            205
attaaacatt tgtttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat    787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa    847
c                                                                    848
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1 5 10

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ctgccatgta catgatagag agattc 26

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name CMYB_01
score 0.983
sequence tgtcagttg
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name MYOD_Q6
score 0.961
sequence cccaactgac
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<222> complement(75..85)

<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag
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name S8_01
score 0.966
sequence aactaaattag
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name DELTAEF1_01
score 0.960
sequence gcacacctcag
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name GATA_C
score 0.964
sequence agataaatcca
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name CMYB_01
score 0.958
sequence cttcagttg
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name GATA1_02
score 0.959
sequence ttgtagataggaca
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name GATA_C
score 0.953
sequence agataggacat
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sequence cataacagatggtaag
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score 0.978
sequence cataacagatggtaag
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name MYOD_Q6
score 0.954
sequence accatctgtt
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<222> complement(302..314)
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name GATA1_04
score 0.953
sequence tcaagataaagta
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name IK1_01
score 0.963
sequence agttgggaattcc
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name IK2_01
score 0.985
sequence agttgggaattc
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name CREL_01
score 0.962
sequence tgggaattcc
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score 0.950
sequence tcagtgatatggca
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name SRY_02
score 0.951
sequence taaaacaaaaca

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<223> matinspector prediction
      name E2F_02
      score 0.957
      sequence tttagcgc
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<222> complement(514..521)
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      score 0.975
      sequence tgaggga
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tgagtgcagt gttacatgtc agttgggtta agtttgttaa tgtcattcaa atcttctatg     60
tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta    120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta    180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa    240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg    300
atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta    360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag    420
catcagtgat atggcaaatg tgggactaag ggtagtgatc agagggttaa aattgtgtgt    480
tttgttttag cgctgctggg gcatcgcctt gggtcccctc aaacagattc ccatgaatct    540
cttcat                                                                546
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<223> oligonucleotide
<400> 32

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gtaccaggga ctgtgaccat tgc                                              23
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<210> 33
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<223> oligonucleotide
<400> 33

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ctgtgaccat tgctcccaag agag                                             24
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<210> 34
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<213> Homo Sapiens
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<221> promoter
<222> 1..806
<220>
<221> transcription start site
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<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction

name NFY_Q6
score 0.956
sequence ggaccaatcat
<220>
<221> protein_bind
<222> 70..77
<223> matinspector prediction
name MZF1_01
score 0.962
sequence cctgggga
<220>
<221> protein_bind
<222> 124..132
<223> matinspector prediction
name CMYB_01
score 0.994
sequence tgaccgttg
<220>
<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
name VMYB_02
score 0.985
sequence tccaacggt
<220>
<221> protein_bind
<222> 135..143
<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa
<220>
<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa
<220>
<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
name MZF1_01
score 0.956
sequence ttgggga
<220>
<221> protein_bind
<222> 357..368
<223> matinspector prediction
name IK2_01
score 0.965
sequence gaatgggatttc
<220>
<221> protein_bind
<222> 384..391
<223> matinspector prediction
name MZF1_01
score 0.986

sequence agagggga
<220>
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<222> complement(410..421)
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name SRY_02
score 0.955
sequence gaaaacaaaaca
<220>
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<222> 592..599
<223> matinspector prediction
name MZF1_01
score 0.960
sequence gaagggga
<220>
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<222> 618..627
<223> matinspector prediction
name MYOD_Q6
score 0.981
sequence agcatctgcc
<220>
<221> protein_bind
<222> 632..642
<223> matinspector prediction
name DELTAEF1_01
score 0.958
sequence tcccaccttcc
<220>
<221> protein_bind
<222> complement(813..823)
<223> matinspector prediction
name S8_01
score 0.992
sequence gaggcaattat
<220>
<221> protein_bind
<222> complement(824..831)
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga
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<223> n=a, g, c or t
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tactataggg cacgcgtggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa 60
tgattggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct 120
cggtgaccgt tggattcctg gaagcagtag ctgttctgtt tggatctggt agggacaggg 180
ctcagagggc taggcacgag ggaaggtcag aggagaaggs aggsarggcc cagtgagarg 240
ggagcatgcc ttcccccaac cctggcttsc ycttggymam agggcgktty tgggmacttr 300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacaa tagcctgaat 360
gggatttcag gttagncagg gtgagagggg aggctctctg gcttagtttt gttttgtttt 420
ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggctt gtcctcaccc 480
agtcggaact ccctaccact ttcaggagag tggttttagg cccgtggggc tgttctgttc 540
caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcggggcc tgaaggggag 600

tgggttctcg cccaaagagc atctgcccat ttcccacctt cccttctccc accagaagct 660
tgcctgagct gtttggacaa aaatccaaac cccacttggc tactctggcc tggcttcagc 720
ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct 780
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tctcttggga gcaatggtca c 861

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<223> oligonucleotide
<400> 35
ctgggatgga aggcacggta 20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 36
gagaccacac agctagacaa 20

<210> 37
<211> 555
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<220>
<221> transcription start site
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<220>
<221> protein_bind
<222> 191..206
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name ARNT_01
score 0.964
sequence ggactcacgtgctgct
<220>
<221> protein_bind
<222> 193..204
<223> matinspector prediction
name NMYC_01
score 0.965
sequence actcacgtgctg
<220>
<221> protein_bind
<222> 193..204
<223> matinspector prediction
name USF_01
score 0.985
sequence actcacgtgctg
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<221> protein_bind
<222> complement(193..204)

<223> matinspector prediction
name USF_01
score 0.985
sequence cagcacgtgagt
<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name NMYC_01
score 0.956
sequence cagcacgtgagt
<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name MYCMAX_02
score 0.972
sequence cagcacgtgagt
<220>
<221> protein_bind
<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc
<220>
<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga
<220>
<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga
<220>
<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct
<220>
<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc
<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4

score 0.963
sequence agtgactgaac
<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac
<220>
<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C
score 1.000
sequence tgtggtctc
<400> 37
ctatagggca cgcktggtcg acggcccggg ctggtctggt ctgtkgtgga gtcgggttga 60
aggacagcat ttgtkacatc tggtctactg caccttccct ctgccgtgca cttggccttt 120
kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga 180
aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta 240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatcc aagtgattgt 300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
gttgctctgc ccatggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
cgtgtcttct gcctgctccc gctcacatcc cacacttgtg ttcagtcact gagttacaga 480
ttttgcctcc tcaatttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc 540
tagctgtgtg gtctc 555

<210> 38
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<220>
<223> oligonucleotide
<400> 38
ggccatacac ttgagtgac 19

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 39
atatagacaa acgcacacc 19

<210> 40
<211> 1098
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 173..211
<223> Von Heijne matrix
score 4.19999980926514
seq MLAVSLTVPLLGA/MM
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<221> polyA_signal

<222> 1063..1068
<220>
<221> polyA_site
<222> 1087..1098
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<221> misc_feature
<222> 144..467
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<220>
<221> misc_feature
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<220>
<221> misc_feature
<222> 436..523
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id :AA057573
est
<220>
<221> misc_feature
<222> 708..786
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<222> 635..682
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<222> 144..506
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id :H12619
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<220>
<221> misc_feature
<222> 90..467
<223> homology
id :T03538
est

<220>
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<222> 314..523
<223> homology
id :T34150
est
<220>
<221> misc_feature
<222> 567..687
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id :T34150
est
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<222> 686..730
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id :T34150
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id :N32314
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id :N32314
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<222> 352..523
<223> homology
id :T77966
est
<220>
<221> misc_feature
<222> 218..351
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id :T77966
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<222> 510..553
<223> homology

id :T77966
est
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<222> 550..917
<223> homology
id :AA464128
est
<220>
<221> misc_feature
<222> 1083
<223> n=a, g, c or t
<400> 40

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agtgaggtgg tttctgcggg tgaggctggc gcccgtacca tgagcgaggc ggacgggctg      60
cgacagcgcc ggcccctgcg gcccgcaagt cgtcacagac gatgatggcc aggccccgga     120
ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg     178
                                                          Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa       226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
    -10                 -5                  1                5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg       274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
                10                  15                  20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg       322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
            25                  30                  35
ttt gaa aat caa ctt gtt gga ccg gag tcc ata gca cat att ggg gat       370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
        40                  45                  50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat       418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
    55                  60                  65
ggt gaa ata gag acc att gcc cgg ttt ggt tcg ggc cct tgc aaa acc       466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
70                  75                  80                  85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg       514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
                90                  95                  100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg       562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
            105                 110                 115
aag taaatccctg gaaacgtgaa gtgaaactgc tgctgtcctc cgagacaccc            615
Lys
attgagggga agaacatgtc ctttgtgaat gatcttacag tcactcagga tgggaggaag     675
atttatttca ccgattctag cagcaaatgg caaagacgag actacctgct tctggtgatg     735
gagggcacag atgacgggcg cctgctggag tatgatactg tgaccaggga agtaaaagtt     795
ttattggacc agctgcggtt cccgaatgga gtccagctgt ctcctgcaga agactttgtc     855
ctggtggcag aaacaaccat ggccaggata cgaagagtct acgtttctgg cctgatgaag     915
ggcggggctg atctgtttgt ggagaacatg cctggatttc cagacaacat ccggcccagc     975
agctctgggg ggtactgggt gggcatgtcg accatccgcc ctaaccctgg gttttccatg    1035
ctggatttct tatctgagag accctggatt aaaaggatga tttttaangg taaaaaaaaa    1095
aaa                                                                 1098
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<210> 41
<211> 855
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 267..371
<223> Von Heijne matrix
score 5.90000009536743
seq LCGLLHLWLKVFS/LK
<220>
<221> polyA_signal
<222> 817..822
<220>
<221> polyA_site
<222> 842..855
<220>
<221> misc_feature
<222> 608..811
<223> homology
id :M85769
est
<400> 41

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acaatcagtt tgccaatacc tcagaaacaa atacctcgga caaatctttc tctaaagacc      60
tcagtcagat actagtcaat atcaaatcat gtagatggcg gcattttagg cctcggacac     120
catccctaca tgacagtgac aatgatgaac tctcctgtag aaaattatat aggagtataa     180
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa     240
gtagcagtgg ttcagcacac tttggt atg ttg act gtt aat gat gta cgt ttc      293
                             Met Leu Thr Val Asn Asp Val Arg Phe
                             -35                 -30
tat aga aat gtc agg tcc aac cat ttc cca ttt gtt cga cta tgt ggt       341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
    -25                 -20                 -15
ctg tta cat tta tgg ctt aaa gtc ttt tct ctt aaa cag tta aaa aaa       389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
-10                 -5                  1               5
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg       437
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
            10                  15                  20
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat              485
Tyr Val Cys Val Phe Ile
        25
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca     545
tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga     605
tatttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg     665
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt     725
cagagaagaa catttaaagg gttaatattt ttgaaacgtt ttcagataat atctatttga     785
ttattgtggc ttctatttga aatgtgtcta aaataaaatg ctgtttattt aaaatgaaaa     845
aaaaaaaaaa                                                            855
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<213> Homo sapiens
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<223> Von Heijne matrix
score 3.5
seq WSPLSTRSGGTHA/CS
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<221> polyA_signal
<222> 1144..1149

<220>
<221> polyA_site
<222> 1165..1176
<220>
<221> misc_feature
<222> 886..1134
<223> homology
id :AA595193
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<220>
<221> misc_feature
<222> 756..894
<223> homology
id :AA595193
est
<220>
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id :AA595193
est
<220>
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<222> 167..367
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id :W81213
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<220>
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<222> 66..172
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<220>
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<222> 429..508
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id :W81213
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id :AA179182
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<221> misc_feature
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id :HUM524F05B
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<220>
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<222> 886..1134
<223> homology
id :AA398156

est
<220>
<221> misc_feature
<222> 756..894
<223> homology
id :AA398156
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<220>
<221> misc_feature
<222> 590,601
<223> n=a, g, c or t
<400> 42

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aacaagccaa ggagccaaga cgagagggac acacggacaa acaacagaca gaagacgtac     120
tggccgctgg actccgctgc ctcccccatc tccccgccat ctgcgcccgg agg atg        176
                                                              Met
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc       224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                 -25                 -20                 -15
ttc tgg agc cct ttg tcc acc agg tcg ggg ggc act cat gcg tgc tcc       272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
                -10                 -5                  1
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc       320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile
        5                   10                  15
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt       368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser
    20                  25                  30
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc       416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro
35                  40                  45                  50
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct       464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro
                55                  60                  65
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca       512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser
            70                  75                  80
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga       560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly
        85                  90                  95
ctg agc aga ttg agt gat gct ggg gca gam adg cct gag ang aaa ggt       608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly
    100                 105                 110
gtt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc       656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro
115                 120                 125                 130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag       712
Pro Pro
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst    772
statctgcct wgtgttcatt ttgytatttt gtgasgtgag acagcaaaga ccaataaaaa    832
catattttat aagaacaaaa ggcytgggtg cctacccgkg tgggggcacw gtgggaagcc    892
ttctgmtagg gtgtcttgtg ctgtrtggyt tgttttgttt gcccctyttat tttgctttgc    952
ttacccagtc ttcccytamt yttggatgst tyttaaccct caggcaaacc tgtgttcccc   1012
ctgtattcag gstytgcttt aaagcaagcc atgaggctgt tggagtttct gtttagggca   1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt   1132
acataaaaat taataaacat tttcaatgat ggaaaaaaaa aaaa                    1176
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<210> 43

<211> 648
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<213> Homo sapiens
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<221> sig_peptide
<222> 460..555
<223> Von Heijne matrix
score 4
seq FSFMLLGMGGCLP/GF
<220>
<221> polyA_signal
<222> 614..619
<220>
<221> polyA_site
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taagactcat gctacaagaa gttaaataag tttcccgaag tcacacagct agcctctcat    180
cccttttcta ctgagaggaa gtggaatgca ctccgacaag gataaggttt tattgtgagc    240
tggccttgga attaaaccac caccaacaca cttttggatt atcagaaggt ggaaggagtg    300
caaatgccag ttacggtgat gcgttcaaca tccttatttc cagtctttat gacgcctttc    360
ctgaatcaca ggtgcattgg ggtgcttcct cctccccagg actcccaccc aactttgtga    420
acacaaccca cttagaggag ttatctcagc acattatga atg ttg ggg acc acg       474
                                           Met Leu Gly Thr Thr
                                                   -30
ggc ctc ggg aca cag ggt cct tcc cag cag gct ctg ggc ttt ttc tcc      522
Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala Leu Gly Phe Phe Ser
        -25                 -20                 -15
ttt atg tta ctt gga atg ggc ggg tgc ctg cct gga ttc ctg cta cag      570
Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro Gly Phe Leu Leu Gln
    -10                 -5                  1               5
cct ccc aat cga tct cct act ttg cct gca tcc acc ttt gcc cat          615
Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser Thr Phe Ala His
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gagagaaggg ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa       111
                   Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys
                       -95                 -90
aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga       159
Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg
    -85                 -80                 -75
gat gga gta cct gtt att aaa gtg gca aat gac aat gct cca gag cat       207
Asp Gly Val Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His
-70                 -65                 -60                 -55
gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa       255
Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln
                -50                 -45                 -40
gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat       303
Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr
            -35                 -30                 -25
aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt       351
Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser
        -20                 -15                 -10
ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc cta gaa       399
Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu
    -5                  1                   5                   10
aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa att       447
Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile
                15                  20                  25
tct taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca            500
Ser
atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct caagaaaggg     560
ccccctttc caacttatac taaagaacta gcatatagat gtaatttata gatagatcag      620
ttgctatatt ttctggtgta aggtctttct tatttagtga gatctaggga taccacagaa     680
atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga     740
ttctattcag tggattagaa tcaaactggt acattgatcc acttgagccg ttaagtgctg     800
ccaattgtac aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa     860
taaggacata tttttcttca gattatgttt tatttctttg cattgagtga ggtacataaa     920
atggcttggt aaaagtaata aaatcagtac aatcactaac tttcctttgt acatattatt     980
ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg ctgctcttta    1040
atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg taaccaatca    1100
gtgttttaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat tctgtttcca    1160
atgttagtat gtatgtaaac atgatagtac agccattttt ttcatatgtg agtaaaaata    1220
aaatagtatt tttaaaagta aaaaaaaaaa a                                   1251

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ggagcagtcc ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc        174
                                           Met Ala Ser Leu Gly
                                                       -20

ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca       222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
                -15                 -10                 -5
ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt       270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
            1               5                   10
gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa       318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu
    15                  20                  25
tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc       366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr
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ctt ctg ggc ctg ccc gct gac atc cak gct gcc cag gcc atg atg gtg      414
Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala Gln Ala Met Met Val
                50                  55                  60
aca tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc      462
Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly
            65                  70                  75
atg ara tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg      510
Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val
        80                  85                  90
gcg gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc      558
Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe
    95                  100                 105
att cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca      606
Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser
110                 115                 120                 125
cca ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac      654
Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
                130                 135                 140
ttg ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc      702
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu
            145                 150                 155
tgc ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc      750
Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala
        160                 165                 170
tac caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa      798
Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln
    175                 180                 185
cct ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat      846
Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr
190                 195                 200                 205
gtg tgaagaacca ggggccagag ctgggggtg gctgggtctg tgaaaaacag            899
Val
tggacagcac cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaaggtg    959
ctgctgaggg tagactgact ttggccattg gattgagcaa aggcagaaat gggggctagt   1019
gtaacagcat gcaggttgaa ttgccaagga tgctcgccat gccagccttt ctgttttcct   1079
caccttgctg ctcccctgcc ctaagtcccc aaccctcaac ttgaaacccc attcccttaa   1139
gccaggamtc agaggatccc tytgccctck ggtttamctg ggactccatc cccaaaccca   1199
ctaatcacat cccactgact gaccctctgt gatcaaagac cctccctctg gctgaggttg   1259
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Met Phe Ala Pro
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Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
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ccc atg ttg ttg ctg att gtt gga ggt tct ttt ggt ctt cgt gag ttt 213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
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Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu
5 10 15 20
gaa aaa aaa ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag 309
Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu
25 30 35
gga agt atc tgt tgaagggcta ctatctttcc ttggcccttc tcccttgttg 361
Gly Ser Ile Cys
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ttgggaaaat caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt 481
gggaagatcc tgacctcctc caaggaagaa atccaggaaa gccttaagac taagacaact 541
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cctgttccac caagtgagag aaggtactta ctcttgtacc tcctgttcag ccaggtgcat 180
taacagacct ccctacagct gtaggaacta ctgtcccaga gctgaggcaa ggggatttct 240

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caggtcattt ggagaacaag tgctttagta gtagtttaaa gtagtaactg ctactgtatt    300
tagtggggtg gaattcagaa gaaatttgaa gaccagatca tgggtggtct gcatgtga      358
atg aac ach ttt gag cca gac agc ctg gct gtc att gct ttc ttc ctc      406
Met Asn Thr Phe Glu Pro Asp Ser Leu Ala Val Ile Ala Phe Phe Leu
    -35                 -30                 -25
ccc att tgg acc ttc tct gcc ctt aca ttt ttg ttt ctc cat cta cca      454
Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro
-20                 -15                 -10                 -5
cca tcc acc agt cta ttt att aac tta gca aga gga caa ata aag ggc      502
Pro Ser Thr Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly
                1                   5                  10
cct ctt ggc ttg att ttg ctt ctt tct ttc tgt gga gga tat act aag      550
Pro Leu Gly Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys
        15                  20                  25
tgc gac ttt gcc cta tcc tat ttg gaa atc cct aac aga att gag ttt      598
Cys Asp Phe Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe
    30                  35                  40
tct att atg gat cca aaa aga aaa aca aaa tgc taatgaagcc atcasgtcaa    651
Ser Ile Met Asp Pro Lys Arg Lys Thr Lys Cys
45                  50                  55
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gaaaaggtca tggggaagca gaggtgattc atggctctgt ggaatttgag gtgaatggtt   1191
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cttctctagc ttacaatgga ccttttttgaa ctgggaaaca ccttgtctgc attcacttta   1311
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gtgagctgct gagatttggg agtctgcgct aggcccgctt ggagttctga gccgatggaa    180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac       229
           Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
                   -30                 -25                 -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt      277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
                -15                 -10                 -5
tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag      325
Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys
            1               5                   10
ggt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata      373
Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile
    15                  20                  25
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac      421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp
30                  35                  40                  45
tgg aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc      469
Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu
                50                  55                  60
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct       518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
            65                  70
gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt cctaatatat    578
acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg    638
atggacaaaa ktaatctktc actaaaggtc atgtaccagg tttttatact tcccagctaa    698
ttccatctgt ggatgaaagt tgcaatgttg gccccccgtat kattttacac cntcgaaata    758
aaaaatgtga ataactgctc caaaaaaaaa aaa                                 791

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ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggtctaatt aattcctctg 180

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gtttgttgaa gcagttacca agaatcttca acccttccc acaaaagcta attgagtaca    240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg    300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt    357
                                                  Met Trp Trp Phe
                                                      -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
        -15                 -10                 -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
    1               5                   10                  15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
                20                  25                  30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc att      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Ile
            35                  40                  45
gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct gaa      597
Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro Glu
        50                  55                  60
gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga ata      645
Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly Ile
    65                  70                  75
ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag gaa aac aac      693
Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Glu Asn Asn
80                  85                  90                  95
cct ttt tgc tgc aca tgt aag tgg agc tgt gct tac ctt tgg tat ggg      741
Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr Leu Trp Tyr Gly
                100                 105                 110
ctc att ata tat gtt tgt tca gac cat cct ttc cta cca aaa tgc agc      789
Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu Pro Lys Cys Ser
            115                 120                 125
cca aaa tcc aat ggc aaa aca agt ctt ctg gat cag act gtt gtt ggt      837
Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln Thr Val Val Gly
        130                 135                 140
tat ctg gtg tgg agt aag tgc act tagcatgctg acttgctcat cagttttgca     891
Tyr Leu Val Trp Ser Lys Cys Thr
    145                 150
cagtggcaat tttgggactg atttagaaca gaaactccat tggaaccccg aggacaaagg    951
ttatgcgctt cacatgatca ctactgcagc agaatggtct atgtcatttt ccttctttgg   1011
ttttttcctg acttacattc gtgattttca gaaaatttcc ttacgggtgg aagccaactt   1071
acatggatta accctctatg acactgcacc ttgccctatt aacaatgaac gaacacggct   1131
actttccags aagatattag atgaaaggat aaaatatttc tgtaantgan ttastgastt   1191
ctcagggant tggggaaang gttcacagaa gttgcttavt tcttcatcrt gaanattttc   1251
aanccactta antcaaggct gacagstaac acgtgatgaa tgctgataat caggaaacat   1311
gaaagaagcc atttgcatag attattytaa aggatatcat caagaagamt attaaaaaca   1371
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tgrsagtgta mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct     180
aacagtccat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga      234
                                      Met Cys Phe Pro Glu His Arg
                                                     -40
aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca      282
Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala
-35                 -30                 -25                 -20
cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc      330
Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala
               -15                 -10                 -5
tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg      378
Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met
           1               5                  10
caa tgatggctct ctcctgctcc aagatgtgca agaggctgac cagggaacct           431
Gln
atatctgtga aatccgcctc aaaggggaga gccaggtgtt caagaaggcg gtggtactgc    491
atgtgcttcc agaggagccc aaaggtacgc aaatgcttac ttaaagaggg gccaaggggc    551
aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaatg ccagcctttg    611
ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt    671
cagaataaaa atakgagtta ttttagttaa kaataaaata ttgataatta ttgtattatt    731
actttaaaca cacttccccc tcacaaaagc cctgtgaagg atgttttgtt cacatataat    791
gtccaaatat gttttggaca catatttatt aaatggaata aatagtamtt gaaccctggc    851
accthtgaca acaaagtcya tgttyttttt actatgccct aatacctths atcagttatc    911
cacattgatg ctacatytgt attttatagg taccctatgt taggtgtttt gggggataga    971
aaagaaataa gcagkycagg ctcagtggct catgcctgta atcctagcat tttgggaggc   1031
tgaggcagca gaamtgcctg agccccaggg ttcaagactg cagtgagcta tgawggcacc   1091
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gtcggctttc ttggtgcctt ggttcatccc taagggtcct aaccggggag ttatcattac    180
catgttggtg acctgttcag tttgctgcta tctcttttgg ctgattgcaa ttctggccca    240
actcaaccct ctctttggac cgcaattgaa aaatgaaacc atctggtatc tgaagtatca    300
ttggccttga ggaagaagac atgctctaca gtgctcagtc tttgaggtca cgagaagaga    360
atgccttcta g atg caa aat cac ctc caa acc aga cca ctt ttc ttg act     410
             Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr
                         -20                 -15                 -10
tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa      458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
                 -5                   1                   5
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt      506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu
         10                  15                  20
tgg tgaattacgt gcctccataa cctgaactgt gccgactcca caaaacgatt           559
Trp
atgtactctt ctgagataga agatgctgtt cttctgagag atacgttact ctctccttgg    619
aatctgtgga tttgaaaatg gctcctgcct tctcacgtgg gaatcagtga agtgtttaga    679
aactgctgca agacaaacaa gactccagtg gggtggtcag taggaaaaca cgttcagagg    739
gaagaaccat ctcaacagaa tcgcaccaaa ctatactttc aggatgaatt tcttctttct    799
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cgcccgtgac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg      170
             Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
                        -25                 -20
cgg gtg ccc ttg tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc      218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                 -10                 -5                  1
gta aag aca ctg ctc cca gta cca agt ttt gaa gat gtt tcc att cct      266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
            5                   10                  15
gaa aaa ccc aag ctt aga ttt att gaa agg gca cca ctt gtg cca aaa      314
Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys
        20                  25                  30
gta aga aga gaa cct aaa aat tta agt gac ata cgg gga cct tcc act      362
Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr
    35                  40                  45
gaa gct acg gag kkk aca gaa ggc aat ttt gca atc ttg gca ttg ggt      410
Glu Ala Thr Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly
50                  55                  60                  65
ggt ggc tac ctg cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc      458
Gly Gly Tyr Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile
                70                  75                  80
aac cgc tct atg gac ccc aag aac atg ttt gcc ata tgg cga gta cca      506
Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro
            85                  90                  95
gcc cct ttc aag ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg      554
Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly
        100                 105                 110
gga ggc aaa ggt gct att gac cac tac gtg aca cct gtg aag gct ggc      602
Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly
    115                 120                 125
cgc mww gww gta gag atg ggt ggg cgt tgt gma ttt gaa gaa gtg caa      650
Arg Xaa Xaa Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln
130                 135                 140                 145
ggt ttc ctt gac cag gtt gcc cac aag ttg ccc tty gca gca aag gct      698
Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala
                150                 155                 160
gtg agc cgc ggg act yta gag aag atg cga aaa gat caa gag gaa aga      746
Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg
            165                 170                 175
gaa mgt aac aac cag aac ccc tgg aca ttt gag cga ata gcc act gcc      794
Glu Xaa Asn Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala
        180                 185                 190
mac atg ctg ggc ata cgg aaa gta ctg agc cca tat gac ttg acc cac      842
Xaa Met Leu Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His
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aag ggg aaa tam tgg ggc aag tty tac atg ccc mam cgt gtg              884
Lys Gly Lys Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
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tttgagtaga tttytgaaaa acgatgttat ttgttgattt aaaaagaaaa cwgtatttttt   1064
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<222> 489..500
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<222> 40..195
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tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt 120
ctgcagacgc gatggataac gtgcagccga aaataaaaca tcgccccttc tgcttcagtg 180
tgaaaggcca cgtgayag atg ctg cgg ctg gat att atc aac tca ctg gta 231
Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
-30 -25 -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa 279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
-15 -10 -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca 327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
1 5 10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc 375
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
15 20 25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa 423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
30 35 40 45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg 479
Val Leu
tattcttcca aaaaaaaaaa a 500

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<221> polyA_site
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<221> misc_feature
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tgaggggcga gggaaaagtt ttcctcaggt gtggtgggga gagggaggcg gatgccggng    120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg    180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat    240
tgaaagagag gctagaagtt ccgcttgcca gcagcctcct tagtagagcg ga atg agt    298
                                                        Met Ser
                                                            -30
aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu
                -25                 -20                 -15
acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct      394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro
            -10                 -5                  1
ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta      442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu
    5                   10                  15
agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg      490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro
20                  25                  30                  35
tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc          535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu
                40                  45                  50
tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg    595
atttctgaaa agaccataca gataaccaca aatatcaaga aagtcgtctt cagtattaag    655
tagaatttag atttaggttt ccttcctgct tcccacctcc ttcgaataag gaaacgtctt    715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa               765
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<223> Von Heijne matrix
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seq KFCLICLLTFIFH/HC
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<221> polyA_signal
<222> 546..551
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<221> polyA_site
<222> 572..584
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gtgcagccgg ggtttggtac cgagcggaga ggagatgcac acggcactcg agtgtgagga    120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg    171
          Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu
          -20                 -15                 -10
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac      219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp
    -5                  1                   5                  10
cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa ttg      267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu
                15                  20                  25
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac      315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr
            30                  35                  40
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc      363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser
        45                  50                  55
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga      411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg
    60                  65                  70
aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt tct      459
Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser
75                  80                  85                  90
cat tta agg tat ttt ggc agt tca aga ggg aaa gca ttt tca ctc aca      507
His Leu Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
                95                  100                 105
taaccaccca gcattcccat aatcatttaa attcagaaaa tcaaaactgt gaccagtgta    567
wtccacaaaa aaaaaaa                                                   584

<210> 56
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<221> sig_peptide
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<221> polyA_signal
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<222> 1374..1387
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<222> 1258..1372
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<220>
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<222> 791..887
<223> homology
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<222> 94..524
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<222> 44..94
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<222> 1258..1372
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id :AA480326
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<222> 1258..1371
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id :AA253214
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<222> 94..268
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<220>
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<222> 946
<223> n=a, g, c or t
<400> 56

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actcccaggc tgggccagca cacccggcag gctctgtcct ggaaacaggc ttcaacgggc     60
ttccccgaaa accttccccg cttctggata tgaavattca agctgcttgc tgagtcctat    120
tgccggctgc tgggagccag gagagccctg aggagtagtc actcagtagc agctgacgcg    180
tgggtccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc      229
           Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val
           -45                 -40                 -35
aac aag tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc      277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe
        -30                 -25                 -20
atc ttc cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt      325
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser
    -15                 -10                 -5
gat gac cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc      373
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```
Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser
1               5                  10                  15
aac gtc tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg      421
Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp
            20                  25                  30
gcc ctg cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg      469
Ala Leu Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met
        35                  40                  45
cac gtg gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat      517
His Val Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His
    50                  55                  60
ggg gag aac agt ggg cgc ctc tac ctg aac ccc ggc aag aar cgg ggt      565
Gly Glu Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly
65                  70                  75                  80
ggg ctc tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg      613
Gly Leu Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val
                85                  90                  95
gac atc gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc      661
Asp Ile Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile
            100                 105                 110
ctc cct cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg      709
Leu Pro Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val
        115                 120                 125
gac tgc ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc      757
Asp Cys Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe
    130                 135                 140
atg gtg gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc      805
Met Val Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu
145                 150                 155                 160
atc tac ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa      853
Ile Tyr Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys
                165                 170                 175
gct caa gcc atg kgc aca ggt cat cac ccc cav gat acc acy ttt tcc      901
Ala Gln Ala Met Xaa Thr Gly His His Pro Xaa Asp Thr Thr Phe Ser
            180                 185                 190
kgc aaa caa gas gac ytc ytt tcg ggk gac ytc atc ttt ctg ggn tca      949
Xaa Lys Gln Xaa Asp Xaa Xaa Ser Gly Asp Xaa Ile Phe Leu Gly Ser
        195                 200                 205
gac agt cat cyt cct ytc tta cca gac cgc ccc cga gac cat gtg aag      997
Asp Ser His Xaa Pro Xaa Leu Pro Asp Arg Pro Arg Asp His Val Lys
    210                 215                 220
aaa acc aty ttg tgaggggctg cctggamtgg tytggcaggt tgggcctgga         1049
Lys Thr Ile Leu
225
tggggaggct ytagcatyty tcataggtgc aacctgagag tgggggagct aagccatgag   1109
gtaggggcag gcaagagaga ggattcagac gytytgggag ccagttccta gtcctcaamt   1169
ccagccacct gccccagsth gacggcamtg ggccagttcc ccctytgsty tgcagstcgg   1229
tttccttttty tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg   1289
ttcatagaag aacacacatg cgggcacctt catygtgtgt ggcccactgt cagaacttaa   1349
taaaagtcaa mtcatttgct ggttaaaaaa aaaaaaaa                           1387

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<222> 1183..1240
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<222> 803..854
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aagccatcca ggggtcttta accagaagag agaggagagc ctcaggagtt aggaccagaa     120
gaagccaggg aagcagtgca atg gct tca aaa atc ttg ctt aac gta caa gag     173
                      Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu
                                  -35                 -30
gag gtg acc tgt ccc atc tgc ctg gag ctg ttg aca gaa ccc ttg agt       221
Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
    -25                 -20                 -15
cta gac tgt ggc cac agc ctc tgc cga gcc tgc atc act gtg agc aac       269
Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn
-10                 -5                  1                   5
aag gag gca gtg acc agc atg gga gga aaa agc agc tgt cct gtg tgt       317
Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys
            10                  15                  20
ggt atc agt tac tca ttt gaa cat cta cag gct aat cag cat cgg gcc       365
Gly Ile Ser Tyr Ser Phe Glu His Leu Gln Ala Asn Gln His Arg Ala
        25                  30                  35
aac ata gtg gag aga ctc aag gag gtc aag ttg agc cca gac aat ggg       413
Asn Ile Val Glu Arg Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly
    40                  45                  50
aag aag aga gat ctc tgt gat cat cat gga gag aaa ctc cta ctc ttc       461
Lys Lys Arg Asp Leu Cys Asp His His Gly Glu Lys Leu Leu Leu Phe
55                  60                  65                  70
tgt aag gag gat agg aaa gtc att tgc tgg ctt tgt gag cgg tct cag       509
```

```
Cys Lys Glu Asp Arg Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln
                75                  80                  85
gag cac cgt ggt cac cac aca ggt cct cac gga gga agt att caa gga      557
Glu His Arg Gly His His Thr Gly Pro His Gly Gly Ser Ile Gln Gly
            90                  95                  100
atg tca gga gaa act cca ggc agt cct caa gag gct gaa gaa gga aga      605
Met Ser Gly Glu Thr Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg
        105                 110                 115
gga gga agc tgagaagctg gaagctgaca tcagagaaga gaaaacttcc              654
Gly Gly Ser
    120
tggaagtatc aggtacaaac tgagagacaa aggatacaaa cagaatttga tcagcttaga    714
agcatcctaa ataatgagga gcagagagag ctgcaaagat tggaagaaga agaaaagaag    774
acgctggata agtttgcaga ggctgaggat gagctagttc agcagaagca gttggtgaga    834
gagctcatct cagatgtgga gtgtcggagt cagtggtcaa caatggagct gctgcaggac    894
atgagtggaa tcatgaaatg gagtgagatc tggaggctga aaaagccaaa aatggtttcc    954
aagaaactga agactgtatt ccatgctcca gatctgagta ggatgctgcr aatgtttaga   1014
ggaactgaca gctgtccggt gctactgggt ggatgtcaca ctgaattcag tcaacctaaa   1074
tttgaatckt gtcctttcag aagatcagag acaagtgata tctgtgccaa tttggccttt   1134
tcagtgttat aattatggtg tkbttgggat cccaatattt btcctsstgg gaaacattac   1194
tgggaagtgg acgtgtccaa gaaaactgcc tggatcctgg gggtatactg tagaacatat   1254
tcccgccata tgaagtatgt tgttagaaga tgtgcaaaty gtcaaaatbt ttacaccaaa   1314
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aaaaaaaaaa a                                                        1385

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<222> 72,93
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agactgggtg cctgggagct gaggcagcca ccgtttcagc ctggccagcc ctctggaccc 180
cgaggttgga ccctactgtg acacacctac c atg cgg aca ctc ttc aac ctc 232
Met Arg Thr Leu Phe Asn Leu
-15
ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag 280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys

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        -10                 -5                  1
tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt      328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser
5                   10                  15                  20
ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct          374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp
                25                  30
caaagctgag agtgtggttc ttgagcatcg cagctactgc tcggcaaagg cccgggacag    434
acactttgct ggggatgtac tgggctatgt cactccatgg aacagccatg gctacgatgt    494
caccaaggtc tttgggagca agttcacaca gatctcaccc gtctggctgc agttgaagag    554
acgtggccgt gagatgtttg aggtcacggg cctccacgac gtggaccaag ggtggatgcg    614
agctgtcagg aagcatgcca agggcctgca catagtgcct cggctcctgt ttgaggactg    674
gacttacgat gatttccgga acgtcttaga cagtgaggat gagatagagg agctgagcaa    734
gaccgtggtc caggtggcaa agaaccagca tttcgatggc ttcgtggtgg aggtctggaa    794
ccagctgcta agccagaagc gcgtgggcct catccacatg ctcacccact tggccgaggc    854
cctgcaccag gcccggctgc tggccctcct ggtcatcccg cctgccatca cccccgggac    914
cgaccagctg ggcatgttca cgcacaagga gtttgagcag ctggcccccg tgctggatgg    974
tttcagcctc atgacctacg actactctac agcgcatcag cctggcccta atgcacccct   1034
gtcctgggtt cgagcctgcg tccaggtcct ggacccggaa gtccaagtgg cgaagcaaaa   1094
tcctcctggg gctcaacttc tatggtatgg actacgcgac ctccaaggat gcccgtgagc   1154
ctgttgtcgg ggccaggtac atccagacac tgaadggacc acaggccccg ggaatggtgt   1214
gggacagcca ggcctcagag cacttcttcg agtacaagaa gagccgcagt gggaggcacg   1274
tcgtcttcta cccaaccctg aagtcyctgc aggtgcgggc tggagctggc ccgggagctg   1334
ggcgttgggg tctctatytg ggagctgggc cagggcctgg actacttyta cgacctgcty   1394
taggtgggca ttgcggcctc cgcggtggac gtgttytttt ytaagccatg gagtgagtga   1454
gcaggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa                     1497

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<221> polyA_site
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<223> homology
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<222> 18..122
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<222> 135..475
<223> homology
id :HUMEST5H12
est
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<222> 1093,1128,1135,1147
<223> n=a, g, c or t
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agtcgtccct gctagtactc cgggctgtgg gggtcggtgc ggatattcag tcatgaaatc      60
agggtaggga cttctcccgc agcgacgcgg ctggcaagac tgtttgtgtt gcgggggccg     120
gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg      173
                            Met Leu Leu Ser Ile Gly Met Leu Met
                                                -30
ctg tca gcc aca caa gtc tac acc atc ttg act gtc cag ctc ttt gca       221
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Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln Leu Phe Ala
-25                 -20                 -15                 -10
ttc tta aac cta ctg cct gta gaa gca gac att tta gca tat aac ttt      269
Phe Leu Asn Leu Leu Pro Val Glu Ala Asp Ile Leu Ala Tyr Asn Phe
                -5                  1                   5
gaa aat gca tct cag aca ttt gat gac ctc ccc gca ara ttt ggt tat      317
Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Xaa Phe Gly Tyr
        10                  15                  20
aga ctt cca gct gaa ggt tta aag ggt ttt tta att aac tca aaa cca      365
Arg Leu Pro Ala Glu Gly Leu Lys Gly Phe Leu Ile Asn Ser Lys Pro
    25                  30                  35
gag aat gcc tgt gaa ccc ata gtg cct cca cca gta aaa gac aat tca      413
Glu Asn Ala Cys Glu Pro Ile Val Pro Pro Pro Val Lys Asp Asn Ser
40                  45                  50                  55
tct ggc act ttc atc gtg tta att ara ara ctt gat tgt aat ttt gat      461
Ser Gly Thr Phe Ile Val Leu Ile Xaa Xaa Leu Asp Cys Asn Phe Asp
                60                  65                  70
ata aag gtt tta aat gca cag aga gca gga tac aag gca gcc ata gtt      509
Ile Lys Val Leu Asn Ala Gln Arg Ala Gly Tyr Lys Ala Ala Ile Val
            75                  80                  85
cac aat gtt gat tct gat gac ctc att agc atg gga tcc aac gac att      557
His Asn Val Asp Ser Asp Asp Leu Ile Ser Met Gly Ser Asn Asp Ile
        90                  95                  100
gag gta cta aag aaa att gac att cca tct gtc ttt att ggt gaa tca      605
Glu Val Leu Lys Lys Ile Asp Ile Pro Ser Val Phe Ile Gly Glu Ser
    105                 110                 115
tca gct agt tct ctg aaa gat gaa ttc aca tak gaa aaa ggg ggc cac      653
Ser Ala Ser Ser Leu Lys Asp Glu Phe Thr Xaa Glu Lys Gly Gly His
120                 125                 130                 135
ctt atc tta gtt cca gaa ttt agt ctt cct ttg gaa tac tac cta att      701
Leu Ile Leu Val Pro Glu Phe Ser Leu Pro Leu Glu Tyr Tyr Leu Ile
                140                 145                 150
ccc ttc ctt atc atr gtg ggc atc tgt ctc atc ttg ata gtc att ttc      749
Pro Phe Leu Ile Xaa Val Gly Ile Cys Leu Ile Leu Ile Val Ile Phe
            155                 160                 165
atg atc aca aaa ttg tcc agg gat aga cat aga gct aga aga aac aga      797
Met Ile Thr Lys Leu Ser Arg Asp Arg His Arg Ala Arg Arg Asn Arg
        170                 175                 180
ctt cgt aaa gat caa ctt aag aaa ctt cct gta cat aaa ttc aag aaa      845
Leu Arg Lys Asp Gln Leu Lys Lys Leu Pro Val His Lys Phe Lys Lys
    185                 190                 195
gga gat gag tat gat gta tgt gcc att tgt ttg gat gag tat gaa gat      893
Gly Asp Glu Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp
200                 205                 210                 215
gga gac aaa ctc aga atc ctt ccc tgt tcc cat gct tat cat tgc aag      941
Gly Asp Lys Leu Arg Ile Leu Pro Cys Ser His Ala Tyr His Cys Lys
                220                 225                 230
tgt gta gac cct tgg cta act aaa acc aaa aaa acc tgt cca gtg tgc      989
Cys Val Asp Pro Trp Leu Thr Lys Thr Lys Lys Thr Cys Pro Val Cys
            235                 240                 245
agg caa aaa gtt gtt cct tct caa ggc gat tca gac tct gac aca gac     1037
Arg Gln Lys Val Val Pro Ser Gln Gly Asp Ser Asp Ser Asp Thr Asp
        250                 255                 260
agt agt caa gaa gaa aat gaa gtg aca gaa cat acc cct tta ctg aga     1085
Ser Ser Gln Glu Glu Asn Glu Val Thr Glu His Thr Pro Leu Leu Arg
    265                 270                 275
cct tta gnc ttc tgt cag tgc cca rgt cam ttt ggg gct tta ntc gga     1133
Pro Leu Xaa Phe Cys Gln Cys Pro Xaa Xaa Phe Gly Ala Leu Xaa Gly
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```
280                 285                 290                 295
ant ccc gct cac ant cag aak cat gac aga atc att cag act ast gag     1181
Xaa Pro Ala His Xaa Gln Xaa His Asp Arg Ile Ile Gln Thr Xaa Glu
                300                 305                 310
gaa gac gac aat gaa gat act gac agt agt gat gca gaa gaa              1223
Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp Ala Glu Glu
            315                 320                 325
tgaaattaat gaacatgatg tcgtggtcca gttgcagcct aatggtgaac gggattacaa   1283
catagcaaat actgtttgac tttcagaaga tgattggttt atttcccttt aaaatgatta   1343
ggtatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt   1403
ttttagtact ytacagttta atcaaattac tgaaacagga cttttgatyt ggtatttatc   1463
tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc   1523
agctyttytt ttggaatgaa agtatagcca aaacaaaaaa aaaaaaa                 1570

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<213> Homo sapiens
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<221> polyA_signal
<222> 976..981
<220>
<221> polyA_site
<222> 1010..1022
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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat      117
                                                        Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt       165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40                 -35                 -30                 -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
                -20                 -15                 -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
            -5                  1                   5
ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga      309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg Leu Gly
    10                  15                  20
cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg      357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu
25                  30                  35                  40
cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc      405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
                45                  50                  55
aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag      453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
            60                  65                  70
gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtg      501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
        75                  80                  85
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gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc      549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
    90                  95                  100
act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct      597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
105                 110                 115                 120
gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc      645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
                125                 130                 135
acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt      693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
            140                 145                 150
cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc      741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
        155                 160                 165
acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt      789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser
    170                 175                 180
gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc      837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro
185                 190                 195                 200
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc      885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr
                205                 210                 215
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag      933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu
            220                 225                 230
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa      981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys
        235                 240                 245
gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaa                      1022
Ala
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<210> 61
<211> 615
<212> DNA
<213> Homo sapiens
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<220>
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<222> 586..591
<220>
<221> polyA_site
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<221> misc_feature
<222> 341..574
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<220>
<221> misc_feature
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<222> 341..574
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<222> 341..574
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<220>
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<221> misc_feature
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<400> 61
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gatcctgcca acattgttca tgactttaac aagaaactta cagcctattt agatcttaac 120
ctggataagt gctatgtgat ccctctgaac acttccattg ttatgccacc cagaaaccta 180
ctggagttac ttattaacat caaggctgga acctatttgc ctcagtccta tctgattc 238

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atg agc aca tgg tta tta ctg atc gca ttg aaa aca ttg atc acc tgg      286
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
    -25                 -20                 -15
gtt tct tta ttt atc gac tgt gtc atg aca agg aaa ctt aca aac tgc      334
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
-10                 -5                  1               5
aac gct aga gaa act att aaa ggt att cag aaa cgt gaa gcc agc aat      382
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
            10                  15                  20
tgt ttc gca att cgg cat ttt gaa aac aaa ttt gcc gtg gaa act tta      430
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
        25                  30                  35
att tgt tct tgaacagtca agaaaaacat tattgaggaa aattaatatc              479
Ile Cys Ser
    40
acagcataac cccacccttt acattttgtg cagtgattat tttttaaagt cttctttcat    539
gtaagtagca aacagggctt tactatcttt tcatctcatt aattcaatta aaaccattac    599
cccaaaaaaa aaaaaa                                                    615
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<210> 62
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<222> 157..345
<223> Von Heijne matrix
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<222> 771..776
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<221> polyA_site
<222> 791..804
<220>
<221> misc_feature
<222> 244..789
<223> homology
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<220>
<221> misc_feature
<222> 286..790
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<220>
<221> misc_feature
<222> 287..790
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<220>
<221> misc_feature
<222> 520..790
<223> homology
id :AA165350

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<220>
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<222> 389..522
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<220>
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<222> 336..386
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<220>
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<222> 326..790
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<223> homology
id :AA428006
est
<400> 62

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aacagcgggc agggaaagcc gcgggaaggg tactccaggc gagaggcgga cgcgagtcgt      60
cgtggcagga aaagtgacta gctccccttc gttgtcagcc agggacgaga acacagccac     120
gctcccaccc ggctgcchaa ggatccctcg gcggcg atg tcg gcc gcc ggt gcc       174
                                        Met Ser Ala Ala Gly Ala
                                                        -60
cga ggc ctg cgg gcc acc tac cac cgg ctc ctc gat aaa gtg gag ctg       222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
        -55                 -50                 -45
atg ctg ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc       270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
    -40                 -35                 -30
aga aca gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt       318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25                 -20                 -15                 -10
gct gga ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct       366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
                -5                  1                   5
caa tct gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca       414
```

```
Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
        10                  15                  20
ctt gta att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt      462
Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe
    25                  30                  35
gtg ggg gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac      510
Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn
40                  45                  50                  55
caa gaa cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc            557
Gln Glu Leu Lys Ala Lys Ala His Lys
                60
tgaacaatct agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa    617
agcaaagcta actgtgtgtt tagaaggcac tgtaactggt agctagttct tgattcaata    677
gaaaaatgca gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg    737
gatattagta acatttttct accatttgtc cgtaataaaa catacttgct cgtaaaaaaa    797
aaaaaaa                                                             804
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<210> 63
<211> 792
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 194..253
<223> Von Heijne matrix
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<220>
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<222> 768..773
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<221> polyA_site
<222> 780..792
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<221> misc_feature
<222> 154..428
<223> homology
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cagccctgct ccctgcagcc aggtgtagtt tcgggagcca ctggggccaa agtgagagtc 120
cagcggtctt ccagcgcttg ggccacggcg gcggccctgg gagcagaggt ggagcgaccc 180
cattacgcta aag atg aaa ggc tgg ggt tgg ctg gcc ctg ctt ctg ggg 229
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly
-20 -15 -10
gcc ctg ctg gga acc gcc tgg gct cgg agg agc cgg gat ctc cac tgt 277
Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys
-5 1 5
gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa att gcc cag 325
Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln
10 15 20
gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg atc aat cca 373
Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro
25 30 35 40
gat ggc agc cag tca gtg gtg gag gta act gtt act gkt tcc ccc aaa 421
Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys
45 50 55
aca aaa gta gct cac tct ggc ttt tgg atg aaa att cga ctg ctt aaa 469
Thr Lys Val Ala His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys

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            60                  65                  70
aaa gga cct tgg tct taatagaaaa tgaagraaaa cagactcaga aaaaaagatt      524
Lys Gly Pro Trp Ser
        75
tbggctctgt ctcawtttgg aagaaggctg gcaggcttat tccccaatgc aactttgctt    584
cctggctgca aaccyttaat acytttgttt ctgctgtaga aatttgttag ccaaaacawg    644
ggagtcctga twcagcaacc ccttcttcca caatccacca tgactggttt ttaatgtamc    704
acttggggta tacatgcaaa accatccgtt cmaaaatctg aatycggagc ttaaaaattt    764
aaaaatgaaa aacchaaaaa aaaaaaaa                                       792

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<221> polyA_site
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<222> 258..553
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<220>
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<222> 258..553
<223> homology
id :AA547310
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<220>
<221> misc_feature
<222> 119..258
<223> homology
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<220>
<221> misc_feature
<222> 359..553
<223> homology
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<220>
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<222> 552..683
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id :AA565602
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<220>
<221> misc_feature
<222> 364..553
<223> homology
id :AA136094
est

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<222> 258..461
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<222> 216..258
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<222> 743
<223> n=a, g, c or t
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ccaaagtgag agtccagcgg tcttccagcg cttgggccac ggcggcggcc ctgggagcag     120
aggtggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg     174
                              Met Lys Gly Trp Gly Trp Leu Ala Leu
                              -20                 -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat       222
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
    -10                 -5                  1               5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga       270
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly
                10                  15                  20
aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg       318
Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro
                25                  30                  35
gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg       366
Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro
        40                  45                  50
ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg        415
Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met
    55                  60                  65
aaggagtatg gggaacagat tgatccttcc acccatcgca agaactacgt acgtgtagtg     475
ggccggaatg gagaatccag tgaactggac ctacaaggca tccgaatcga ctcagatatt     535
agcggcaccc tcaagbtttg cgtgtgggaa cattgtggag gaatacgagg atgaactcat     595
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tgaatcttt tcccgagagg ctgacaatgt taaagacaaa ctttgcagta agcgaacaga 655
tctttgtgac catgccctgc acatatcggc atgatgagct atgaaccact ggagcagccc 715
acactggctt gatggatcac ccccaggnaa gggaaaatgg tggcaatgcc ttttatatat 775
tatgttttac tgaaattaac tgaaaaatat gaaaccaaaa gtscaaaaaa aaaaaaa 832

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<213> Homo sapiens
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<222> 706..711
<220>
<221> polyA_site
<222> 709..721
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id :H98648
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id :AA594850
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<221> misc_feature
<222> 165..474
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<222> 1..74
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<222> 270..349
<223> homology
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<220>
<221> misc_feature
<222> 213..261
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<220>
<221> misc_feature
<222> 165..214
<223> homology
id :AA186657

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<221> misc_feature
<222> 346..387
<223> homology
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<222> 52..400
<223> homology
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<221> misc_feature
<222> 398..436
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<221> misc_feature
<222> 171..316
<223> homology
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ccctgcagtt cgcggwacag tctctattag agcgcgtgta tagaggcaga kaggagtgaa    120
gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc       173
                                        Met Pro Ala Gly Val Pro
                                        -25                 -20
atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc      221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
                -15                 -10                 -5
gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata      269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
            1               5                   10
cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga      317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
    15                  20                  25
ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt      365
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
30                  35                  40                  45
aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc           418
Lys
ttaatttatt gcatcaaact acttgtcctt aagcacttag tctaatgcta actgcaagag    478
gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt    538
tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg    598
tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt    658
atttcatata aattaagaaa ttatttaaaa actatgaact aggtttcatt aaaaaaaaaa    718
gaa                                                                 721

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<221> polyA_site
<222> 518..531
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<223> homology
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<222> 85..207
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<220>
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<222> 202..517
<223> homology
id :AA074748
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<220>
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<222> 116..153
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<220>
<221> misc_feature
<222> 167..202
<223> homology
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<222> 258..517
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<222> 28..227
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<222> 265..310
<223> homology

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<222> 227..263
<223> homology
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<221> misc_feature
<222> 352..385
<223> homology
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aggaagttga aaggcccaga ggaggcctcc gggcaaatgg ccggagctgg accgaccatg     120
ctgctacgag aagagaatgg ctgttgcagt cggcgtcaga gcagctccag tgccggggat     180
tcggacggag agcgcgagga ctcggcggct gagcgcgccc gacagcagct agaggcgctg     240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tcg gct        292
                                   Met Asp Gly His Trp Ser Ala
                                               -40
gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc       340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                 -30                 -25                 -20
agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg       388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
                -15                 -10                 -5
tgc tgg gcc tgg cca tgg tac ccg gac acc aca tcg ttt cca ttg agg       436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg
            1               5                   10
tgc aga ggg aga gtc tgaccgggcc tccgtatctc tgaccacgat ggcgcttacc      491
Cys Arg Gly Arg Val
    15
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa                           531

<210> 67
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<213> Homo sapiens
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<223> Von Heijne matrix
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     seq LELLTSCSPPASA/SQ
<220>
<221> polyA_signal
<222> 736..741
<220>
<221> polyA_site
<222> 770..783
<220>
<221> misc_feature
<222> 207..263
<223> homology
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     est
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agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac     120
ccggggtagg gtttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc      180
ggatggcgga gacgaaggac gcagcgcaga tgttggtgac cttcaaggat gtggctgtga     240
cctttacccg ggaggagtgg agacagctgg acctggccca gaggaccctg taccgagagg     300
tgatcgggtt cccaaaccag agttggtcca cctgctagag catgggcagg agctgtggat     360
agtgaagaga ggcctctcac atg cta cct gtg cag agt ttc act ctt gtt gcc     413
                      Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala
                                      -80                 -75
cag gct gga gtg cag tgg cgc cat ctc agc tca ctg caa ctt ctg cct       461
Gln Ala Gly Val Gln Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro
        -70                 -65                 -60
ccc gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat       509
Pro Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
    -55                 -50                 -45
tac agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta       557
Tyr Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val
-40                 -35                 -30                 -25
gag acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc       605
Glu Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr
                -20                 -15                 -10
tca tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc       653
Ser Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly
            -5                  1               5
gtg agc cac gtg ccc ggc aaa aaa aaa ctg ctt aag gtt gaa aag aaa       701
Val Ser His Val Pro Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys
    10                  15                  20
aat tta aga aaw ttg ctg acg gra ata aaa acy taataaaact accacccgaa     754
Asn Leu Arg Xaa Leu Leu Thr Xaa Ile Lys Thr
25                  30                  35
ggaatgaaaa aaccaaaaaa aaaaaaaaa                                       783

<210> 68
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<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
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<221> polyA_signal
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<220>
<221> polyA_site
<222> 984..996
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<222> 676..959
<223> homology
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<220>
<221> misc_feature
<222> 609..679
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<220>
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<222> 225..433
<223> homology
id :AA398040
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<220>
<221> misc_feature
<222> 433..563
<223> homology
id :AA398040
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<400> 68
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ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg 120
gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc 172
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
-20 -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc 220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10 -5 1 5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt 268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
10 15 20
gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag 316
Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
25 30 35
gta tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt 364
Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu
40 45 50
ttt taaactttct ttcattgact cttaagtgca gggctagaac acggggaaca 417
Phe
tacctgcttg cctcaaacta aaggatctag tcmtytctga aktcctctac tsacrrttra 477
caacaatatc ctgtgcaaaa ttttgcgaaa gaaatgaaat acaattgcmg cgtgcatcga 537
cattttgga agtagagatt aacyyttcgt atttttactt cmtcgaagtt aagttccaaa 597
tgtgtatgtg ttaagtaaat gttttcagta aytgggaaag ataaagtgta atccaattta 657
agtttgtgaa aatgagtaat tccgtatcca aaytggagtt aacaccaaag tattgtacaa 717
attgcttgca cagttggtcc gtacacaata gacaggctyt gtatttttag ctgacgttgt 777
tatttgatga tgatgtactc cattttcamt acggcccgaa gagamtagta atcctccttg 837
tagtagatgt ttttgtcttg aaagtatctt ttaaatgtyt gagcacttta aggaacagac 897
ccttattaat gtyttttaag ttttattcaa tttccagtca caaatatttt atggtatttg 957
attgtytaat aaatttgtat gatattaaaa aaaaaaaaa 996

<210> 69
<211> 657
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 183..338
<223> Von Heijne matrix
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seq VMLETCGLLVSLG/QS
<220>
<221> polyA_signal

<222> 620..625
<220>
<221> polyA_site
<222> 644..657
<220>
<221> misc_feature
<222> 207..263
<223> homology
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agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac 120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgtcct gccaacggtc 180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag 227
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
-50 -45 -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-35 -30 -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt 323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
-20 -15 -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag 371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
-5 1 5 10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag 419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
15 20 25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag 467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
30 35 40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt 527
gtcctcaggc tggctcctca tagggatgct gggtgctgca gccttgactg gggcagcagg 587
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aaaaaaaaaa 657

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gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc     172
                    Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                        -20                 -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
    -10                 -5                  1               5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                10                  15                  20
gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
            25                  30                  35
tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt      364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe
        40                  45                  50
gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a       416
Val Thr Glu Glu Gly Arg Asn
    55                  60

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cagccccaag agtggaggct gccacatcct aacatasgta tctattgaaa aggaagcagt    120
gtgtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca tgt agc     170
         Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser
             -15                 -10                 -5
aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt ctc ccc      218
Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro
        1               5                   10
agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc tgc agg      266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
15                  20                  25                  30
cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc ctc cac      314
Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His
                35                  40                  45
ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc tgg gac      362
Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp
            50                  55                  60
tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact gtcttccttt    415
Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
        65                  70
cccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct cccttgccct    475
ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa gtgaaaaaaa    535
aaaaaaaa                                                             543

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tgactccctg gtggtgtgcg aggtagaccc agagctaaca gaaaagctga kgaaattccg 120
cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaag accggcagat 180

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ggtggtgctg gaggaagaat ttcagaacat ttccccagag gagctcaaaa tggagttgcc    240
ggagagacag cccaggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc    296
                                                  Met Thr Met Ala
gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca     344
Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
-15                 -10                 -5                   1
agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga       394
Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
            5                   10
cagcagagct cacaaaggtg ttcgaaatcc gcaccactga tgacctcact gaggcctggc    454
tccaagaaaa gttgtctttc tttcgttgat ctctgggctg gggactgaat tcctgatgtc    514
tgagtcctca aggtgactgg ggacttggaa cccctaggac ctgaacaacc aaggacttta    574
aataaatttt aaaatgcaaa aaaaaaaaaa a                                   605
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ggattccagc cattgctgca gctgctccac agccctttc aggacccaaa caaccgcagc    120
cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc     171
                Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
                               -100                -95
tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa      219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
    -90                 -85                 -80
gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag      267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-75                 -70                 -65                 -60
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc      315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
                -55                 -50                 -45
aca ggt aac ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc      363
Thr Gly Asn Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg
            -40                 -35                 -30
ggg gac tat gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat      411
Gly Asp Tyr Asp Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr
        -25                 -20                 -15
gcc ttc tta ggc ttg aca gcc cca tct ggt tca aag gaa gca gga agg      459
Ala Phe Leu Gly Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg
    -10                 -5                  1                   5
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tgc aag caa agc agc aag cca tgaaccttga gcactgtgct tttaagcatc 510
Cys Lys Gln Ser Ser Lys Pro
10
ctgaaaaatg agtctccatt gcttttataa aatagcagaa ttagctttgc sttcaaaaga 570
aataggstta atgttgaaat aatagattag ttgggttttc acatgcaaac amtcaaaatg 630
aatacaaaat taaaatttga acattatggt gattatggtg aggagaatgg gatattaaca 690
taaaattata ttaataagta gatatygtag aaatagtgtt gttacctgcc aagccatcct 750
gtatacacca atgattttac aaagaaaaca cccttccctc cttytgccat tamtatggca 810
acctaagtgt atytgcagct ttacattaaa aaggagaaag agaaaaaaaa aaaa 864

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tgcgagagaa gggggttcat catggcggat gacctaaagc gattcttgta taaaaagtta     180
ccaagtgttg aagggctcc atg cca ttg ttg tgt cag ata gag atg gag tac      232
                     Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
                        -75                 -70
ctg tta tta aag tgg caa atg aca atg ctc cag agc atg ctt tgc gac      280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                 -60                 -55                 -50
ctg gtt tct tat cca ctt ttg ccc ttg caa cag acc aag gaa gca aac      328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
                -45                 -40                 -35
ttg gac ttt cca aaa ata aaa gta tca tct gtt act ata aca cct acc      376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
            -30                 -25                 -20
agg tgg ttc aat tta atc gtt tac ctt tgg gtg gtg agt ttc ata gcc      424
Arg Trp Phe Asn Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
        -15                 -10                 -5
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt      472
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
    1               5                   10                  15
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct              514
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
                20                  25
taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc     574
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg ccccttttc      634
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt     694
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tggatcagaa tcaaactggt acattgatcc acttgagccg ttaagtgctg ccaattgtac 874
aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa taaggacata 934
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Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys
-20 -15 -10
cta gca ctg cag ctg gtg cct ggg agt ccc aag cag cgt gtt ctg aag 157
Leu Ala Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys
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tat atc ttg gaa cct cca ccc tgc ata tca gca cct gaa aac tgt act 205
Tyr Ile Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr
10 15 20
cac ctg tgt aca atg cag gaa gat tgc gag aaa gga ttt cag tgc tgt 253
His Leu Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys
25 30 35 40
tcc tcc ttc tgt ggg ata gtc tgt tca tca gaa aca ttt caa aag cgc 301
Ser Ser Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg
45 50 55
aac aga atc aaa cac aag ggc tca gaa gtc atc atg cct gcc aac 346
Asn Arg Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
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aaggtattga gaagcaagaa actggaggcc caatatctaa cctgcaaatc gtttttgagt 466
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ttgacttgct ggtgaaggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac 120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag 180
tctgaagagc agccagtgtt tcggcttgtg ccctgtatac ttgaagctgc caaacaagta 240
cgttctgaaa atccagaatg gcttgatgtt tac atg cac att tta caa ctg ctt 294
Met His Ile Leu Gln Leu Leu
-40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act 342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35 -30 -25 -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc 390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
-15 -10 -5
tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg 438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val
1 5 10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act 486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
15 20 25
gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac 534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp
30 35 40 45
agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca 582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro
50 55 60
gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt 630
Glu Asn Ser Ala Gly Val
65
aacccaagat gatttccact tgaaaatctt aaaaggatat tgttatggtg aagtttctgt 690
ctaataattt ttcaggcatt aacaaaggag acggtggctc agggagtaaa ggaaggccgt 750
tgagcaaaca gaagtgttcc tctgcaattt caaaarcctt cttctttcta tagcccctgt 810
gggtggaaga ttttattaaa atcctacgtg aagttgataa ggcgcttgct kgatgacttg 870
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sstgtbcaag aaaataaact ttatttttct cactgaaaaa aaaaaaaa 978

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gaaaccagaa gaaaaatatg agacggggaa tcatcgtgtg atgtgtgtgc tgcctttggc    120
tkwgtgtgtk gaagtycckg ctcaggtgtt aggtacagtg tgtttgatcg tggtggcttg    180
aggggaaccc gctgttcaga gctgtgactg cggctgcact cagagaagct gcccttggct    240
gctcgtagcg ccgggccttc tctcctcgtc atcatccaga gcagccagtg tccgggaggc    300
agaagatgcc ccactccagc ctctggactg ggggctctct tcagtggctg aatgtccagc    360
agagctattt ccttccacag ggggccttgc agggaagggt ccaggacttg acatcttaag    420
atg cgt ctt gtc ccc ttg ggc cag tca ttt ccc ctc tct gag cct cgg      468
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15                 -10                 -5                  1
tgt ctt caa cct gtg aaa tgg gat cat aat cac tgc ctt acc tcc ctc      516
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
            5                   10                  15
acg gtt gtt gtg agg act gag tgt gtg gaa gtt ttt cat aaa ctt tgg      564
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
        20                  25                  30
atg cta gtg taaaaaaaaa aaaa                                         587
Met Leu Val
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<222> 387..400
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tctgactcca tggaaaccag atggggcaac ggggtggttc tagtgcagac tgtagctgca    120
gctcctctcc acctctagcc tgctcatttc cagctcagaa attctactaa tggcgttttt    180
tcttcctgaa aaaggaa atg aac agg gtc cct gct gat tct cca aat atg        230
                  Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
                      -25                 -20
tgt cta atc tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca      278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
    -15                 -10                 -5
aaa atc tgt aga aga gca ttc cag gaa gag gga aga gca aat gca aag      326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys
1               5                   10                  15
acg ggc gtg aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc       375
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Thr Gly Val Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
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ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga cagccaggag cggttttctg     120
ggaactgtgg gatgtgccct tgggggcccg agaaaacaga aggaag atg ctc cag        175
                                                   Met Leu Gln
                                                       -20
acc agt aac tac agc ctg gtg ctc tct ctg cag ttc ctg ctg ctg tcc       223
Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
            -15                 -10                 -5
tat gac ctc ttt gtc aat tcc ttc tca gaa ctg ctc caa aag act cct       271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
        1               5                   10
gtc atc cag ctt gtg ctc ttc atc atc cag gat att gca gtc ctc ttc       319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
15                  20                  25                  30
aac atc atc atc att ttc ctc atg ttc ttc aac acc tcc gtc ttc cag       367
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Val Phe Gln
                35                  40                  45
gct ggc ctg gtc aac ctc cta ttc cat aag ttc aaa ggg acc atc atc       415
Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly Thr Ile Ile
            50                  55                  60
ctg aca gct gtg tac ttt gcc ctc agc atc tcc ctt cat gtc tgg gtc       463
Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His Val Trp Val
        65                  70                  75
atg aac tta cgc tgg aaa aac tcc aac agc ttc ata tgg aca gat gga       511
Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp Thr Asp Gly
    80                  85                  90
ctt caa atg ctg ttt gta ttc cag aga cta gca gca gtg ttg tac tgc       559
Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val Leu Tyr Cys
95                  100                 105                 110
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tac ttc tat aaa cgg aca gcc gta aga cta ggc gat cct cac ttc tac      607
Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro His Phe Tyr
                115                 120                 125
cag gac tct ttg tgg ctg cgc aag gag ttc atg caa gtt cga agg          652
Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val Arg Arg
            130                 135                 140
tgacctcttg tcacactgat ggatactttt ccttcctgat agaagccaca tttgctgctt    712
tgcagggaga gttggcccta tgcatgggca aacagctgga ctttccaagg aaggttcaga    772
ctagctgtgt tcagcattca agaaggaaga tccccccctct tgcacaatta gagtgtcccc   832
atcggtctcc agtgcggcat cccttccttg ccttctacct ctgttccacc cccttccttc    892
ctctcctctc tgtaccattc attctccctg accggccttt cttgccgagg gttctgtggc    952
tcttaccctt gtgaagcttt tcctttagcc tgggacagaa ggacctcccg gcccccaaag   1012
gatctcccag wtgaccaaag gatgcgaaga gtgatagtta cgntgctcct gactgatcac   1072
accgcagaca tttagatttt tatacccaag gcactttaaa aaaatgtttt ataaatagag   1132
aataaattga attyttgttc caaaaaaaaa aaaa                               1166

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<222> 725
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ggcctgctgg gcttggcaac gagggactcg gcctcggagg cgacccagac cacacagaca    120
ctgggtcaag gagtaagcag aggataaaca actggaagga gagcaagcac aaagtcatc     179
atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      227
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
            -65                 -60                 -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      275
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
        -50                 -45                 -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      323
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
    -35                 -30                 -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      371
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20                 -15                 -10                 -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      419
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
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                1               5                   10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      467
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
        15                  20                  25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      515
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
    30                  35                  40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt ccw aca gca              557
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala
45                  50                  55
taacaggcac tgcctcctta cctgtgagga atgcaaaata aagcatggat taagtgagaa    617
gggagactct cagccttcag cttcctaaat tctgtgtctg tgactttcga agtttttaa     677
acctctgaat ttgtacacat ttaaaatttc aaggtgtact ttaaaatnaa aatacttcta    737
atgtvaaaaa aaaaaaa                                                  754

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tccagctctt ccgaagttcg ttcttgcgca aagcccaaag gctggaaaac cgtccacg      178
atg acc agc atg act cag tct ctg cgg gag gtg ata aag gcc atg acc      226
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                 -35                 -30                 -25
aag gct cgc aat ttt gag aga gtt ttg gga aag att act ctt gtc tct      274
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
                -20                 -15                 -10
gct gct cct ggg aaa gtg att tgt gaa atg aaa gta gaa gaa gag cat      322
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
            -5                  1                   5
acc aat gca ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta      370
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
    10                  15                  20
gat aac ata tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc      418
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25                  30                  35                  40
gga gtc agt gtc gat atg aac ata acg tac atg tca cct gca aaa tta      466
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
                45                  50                  55
gga gag gat ata gtg att aca gca cat gtt ctg aag caa gga aaa aca      514
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Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
            60                  65                  70
ctt gca ttt acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta      562
Leu Ala Phe Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu
        75                  80                  85
ata gca caa gga aga cac aca aaa cac ctg gga aac tgagagaaca          608
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
    90                  95                  100
gcagaatgac ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt   668
gtaatttttg aaataaacta gcaaaaccaa aaaaaaaaaa g                       709

<210> 82
<211> 243
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      seq ILFNLLIFLCGFT/NY
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<221> polyA_signal
<222> 211..216
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<222> 230..243
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<223> homology
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<223> homology
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<220>
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id :AA601071
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<221> misc_feature
<222> 200..229
<223> homology
id :AA225190
est
<400> 82

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aactcagtgg caacacccgg gagctgtttt gtcctttgtg gagcctcagc agttccctct     60
ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc       114
                                           Met Gln Cys Phe Ser
                                                           -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
                -15                 -10                 -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
            1               5                   10
cat aaa cct gtt aca atg taaaaaaaaa aaaaa                              243
His Lys Pro Val Thr Met
    15
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<210> 83
<211> 829
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<213> Homo sapiens
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<222> 346..408
<223> Von Heijne matrix
score 5.5
seq SFLPSALVIWTSA/AF
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<222> 792..797
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<221> polyA_site
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<220>
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<220>
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<222> 122..399
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<222> 393..434
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<221> misc_feature
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<223> homology
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<221> misc_feature
<222> 118..399
<223> homology
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<220>
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<223> homology

id :W02860
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<220>
<221> misc_feature
<222> 268..545
<223> homology
id :N44490
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<220>
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<222> 115
<223> n=a, g, c or t
<400> 83

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actcctttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc     60
ctgatgccga gttccgtctc tcgcgtcttt tcctggtccc aggcaaagcg gasgnagatc    120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggtctaatt aattcctctg    180
gtttgttgaa gcagttacca agaatcttca acccttccc acaaaagcta attgagtaca     240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg    300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt    357
                                                Met Trp Trp Phe
                                                    -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
        -15                 -10                 -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
    1               5                   10                  15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
            20                  25                  30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
        35                  40                  45
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaaa           602
Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt    662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata    722
tggtaaggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg    782
gtaagttgaa ataaaatgat watgagagtg acacavaaaa aaaaaaa                  829
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<210> 84
<211> 674
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<222> 194..592
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<222> 187..592
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<220>
<221> misc_feature
<222> 594..661
<223> homology
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<220>
<221> misc_feature
<222> 188..592
<223> homology
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<220>
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<222> 594..661
<223> homology
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<222> 194..444
<223> homology
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<222> 1..102
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<220>
<221> misc_feature
<222> 99..187
<223> homology
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<222> 437..592
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      est
<220>
<221> misc_feature
<222> 594..661
<223> homology
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<220>
<221> misc_feature
<222> 441..592
<223> homology
       id :AA554685
      est
<220>
<221> misc_feature
<222> 594..661
<223> homology
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      est
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<221> misc_feature
<222> 414..503
<223> homology
       id :AA215595
      est
<220>
<221> misc_feature
<222> 510..539
<223> homology
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<400> 84
ataagtgaac cagaccaccc tgatggcatc cacagtgatg tcaaggttgg ggctggccag     60
gggtgggtgg actagaagca tttgggagta gtggccaggg gccctggacg ctagccacgg    120
agctgctgca cagagcctgg tgtccacaag cttccaggtt ggggttggag cctggg atg    179
                                                               Met
agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct gac      227
Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser Asp
            -15                 -10                 -5
ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt ctc      275
Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu
         1               5                  10
atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc aag      323
Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys
15                  20                  25                  30
agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt gta      371
Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val Val
                35                  40                  45
aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca tgagtcgatg       420
Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
            50                  55
ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg tcgaaaataa    480
gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt attgattaag    540
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ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt agggaacata 600
gcaaggggc tcctctgttg gagtaatgta aattgtaatt ataaataaac atgcaaacct 660
ttaaaaaaaa aaaa 674

<210> 85
<211> 478
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 179..319
<223> Von Heijne matrix
score 5.5
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<221> polyA_site
<222> 465..478
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<222> 2..464
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<221> misc_feature
<222> 8..464
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<220>
<221> misc_feature
<222> 2..416
<223> homology
id :AA401411
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<220>
<221> misc_feature
<222> 2..349
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<220>
<221> misc_feature
<222> 126..273
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<220>
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<222> 2..147
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<222> 293..349
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<222> 332..385
<223> homology
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<220>
<221> misc_feature
<222> 163..420
<223> homology
id :AA555127
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<400> 85
aagtccttcg cgccctcctc gccctcccca ccgacatcat gctccagttc ctgcttggat 60
ttacactggg caacgtggtt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg 120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc 178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct 226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
-45 -40 -35
ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct 274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
-30 -25 -20
cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt 322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
-15 -10 -5 1
aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca 370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
5 10 15
aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc 418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
20 25 30
taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa 478

<210> 86
<211> 952
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
score 7.19999980926514
seq ILFSLSFLLVIIT/FP
<220>
<221> polyA_signal
<222> 910..915

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<220>
<221> polyA_site
<222> 940..952
<400> 86
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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat     117
                                                         Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40                 -35                 -30                 -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
                -20                 -15                 -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
            -5                  1               5
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt              310
Leu Lys Ile
    10
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg    370
taactactca ggtagatgga gttgtctatt acagaatcta tagtgctgtc tcagcagtgg    430
ctaakgtcaa cgatgtccat caagcaacat ttctgctggc tcaaaccact ctgagaaatg    490
tcktagggac acaggacctt gtccccagat cttaggctgg acgagaagag atcgcccata    550
agcatccaga ctktacttga tgatgccacc gaactggtgg gggatccggg tggcccgagt    610
ggaaatcaaa gatgttcgga ttcccgtgca gttgcagaga tccatggcag ccgaggstga    670
ggccacccgg gaagsgagag ccaaggtcct tgcagctgaa ggagaaatga atgsttccaa    730
atccctgaag tcagcctcca tggtgstggs tgagtytccc atagctytcc agstgsgsta    790
cctgcagacc ttgagcacgg tagccaccga gaagaatttt acgattgtgt ttcctbtgcc    850
catgaatata ctagagggca ttggtggcgt cagstatgat aaccacaaga agsttbscaa    910
ataaagcctg aggtcybctt gcggtagtca aaaaaaaaaa aa                       952

<210> 87
<211> 131
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -13..-1
<400> 87
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
            -10                 -5                  1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
    5                   10                  15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20                  25                  30                  35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
                40                  45                  50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
            55                  60                  65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
        70                  75                  80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
    85                  90                  95
Gly Arg Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp
100                 105                 110                 115
Tyr Leu Lys

<210> 88
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<211> 63
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -35..-1
<400> 88

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Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35                 -30                 -25                 -20
His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
                -15                 -10                 -5
Val Phe Ser Leu Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu
            1                   5                   10
Phe Glu Ser Cys Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile
    15                  20                  25
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<210> 89
<211> 163
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -31..-1
<220>
<221> UNSURE
<222> 91,108,109,112,124
<223> Xaa = any one of the twenty amino acids
<400> 89

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Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
    -30                 -25                 -20
Ser Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys
-15                 -10                 -5                  1
Ser Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn
            5                   10                  15
Ile Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro
        20                  25                  30
Ser Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys
    35                  40                  45
Pro Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp
50                  55                  60                  65
Pro Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr
                70                  75                  80
Ser Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg
            85                  90                  95
Gly Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys
        100                 105                 110
Gly Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr
    115                 120                 125
Pro Pro Pro
130
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<210> 90
<211> 52
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1

<400> 90
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
-30 -25 -20
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
-15 -10 -5
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1 5 10 15
Thr Phe Ala His
20

<210> 91
<211> 124
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -97..-1
<400> 91
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
-95 -90 -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
-80 -75 -70
Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
-65 -60 -55 -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
-45 -40 -35
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
-30 -25 -20
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
-15 -10 -5
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
1 5 10 15
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile Ser
20 25

<210> 92
<211> 230
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -24..-1
<220>
<221> UNSURE
<222> 54,79
<223> Xaa = any one of the twenty amino acids
<400> 92
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
-20 -15 -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
-5 1 5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
10 15 20
Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
25 30 35 40
Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Ala
45 50 55
Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile

```
            60                  65                  70
Ile Ser Val Val Gly Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg
        75                  80                  85
Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
    90                  95                  100
Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
105                 110                 115                 120
Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
                125                 130                 135
Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile
            140                 145                 150
Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser
        155                 160                 165
Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser
    170                 175                 180
Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr
185                 190                 195                 200
Ser Leu Thr Gly Tyr Val
                205
```

<210> 93
<211> 72
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1
<400> 93

```
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
        -30                 -25                 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
    -15                 -10                 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1               5                   10                  15
Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
            20                  25                  30
Ser Glu Tyr Glu Gly Ser Ile Cys
        35                  40
```

<210> 94
<211> 91
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -36..-1
<400> 94

```
Met Asn Thr Phe Glu Pro Asp Ser Leu Ala Val Ile Ala Phe Phe Leu
    -35                 -30                 -25
Pro Ile Trp Thr Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro
-20                 -15                 -10                 -5
Pro Ser Thr Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly
                1                   5                   10
Pro Leu Gly Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys
        15                  20                  25
Cys Asp Phe Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe
    30                  35                  40
Ser Ile Met Asp Pro Lys Arg Lys Thr Lys Cys
```

45 50 55

<210> 95
<211> 106
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1
<400> 95

```
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
        -30                 -25                 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
    -15                 -10                 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Gly Lys Met
1               5                   10                  15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
            20                  25                  30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
        35                  40                  45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
    50                  55                  60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65                  70
```

<210> 96
<211> 172
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -21..-1
<400> 96

```
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
    -20                 -15                 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5                  1                   5                   10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
            15                  20                  25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
        30                  35                  40
Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
    45                  50                  55
Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
60                  65                  70                  75
Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
                80                  85                  90
Gln Glu Asn Asn Pro Phe Cys Cys Thr Cys Lys Trp Ser Cys Ala Tyr
            95                  100                 105
Leu Trp Tyr Gly Leu Ile Ile Tyr Val Cys Ser Asp His Pro Phe Leu
        110                 115                 120
Pro Lys Cys Ser Pro Lys Ser Asn Gly Lys Thr Ser Leu Leu Asp Gln
    125                 130                 135
Thr Val Val Gly Tyr Leu Val Trp Ser Lys Cys Thr
140                 145                 150
```

<210> 97
<211> 56

<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 97
Met Cys Phe Pro Glu His Arg Arg Gln Met Tyr Ile Gln Asp Arg Leu
-40 -35 -30
Asp Ser Val Thr Arg Arg Ala Arg Gln Gly Arg Ile Cys Ala Ile Leu
-25 -20 -15
Leu Leu Gln Ser Gln Cys Ala Tyr Trp Ala Leu Pro Glu Pro Arg Thr
-10 -5 1 5
Leu Asp Gly Gly His Leu Met Gln
10

<210> 98
<211> 46
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 98
Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr Cys Leu Phe
-20 -15 -10
Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu Cys Leu Ile
-5 1 5 10
Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu Trp
15 20

<210> 99
<211> 251
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -28..-1
<220>
<221> UNSURE
<222> 54,131,132,140,179,194,213,221
<223> Xaa = any one of the twenty amino acids
<400> 99
Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
-25 -20 -15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
-10 -5 1
Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
5 10 15 20
Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
25 30 35
Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
40 45 50
Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr
55 60 65
Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
70 75 80
Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe
85 90 95 100

```
Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys
                  105                 110                 115
Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Xaa Xaa
              120                 125                 130
Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln Gly Phe Leu
          135                 140                 145
Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg
      150                 155                 160
Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Xaa Asn
165                   170                 175                 180
Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Xaa Met Leu
                  185                 190                 195
Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys
              200                 205                 210
Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
          215                 220

<210> 100
<211> 77
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -30..-1
<400> 100
Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
-30                  -25                 -20                 -15
Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
                  -10                 -5                  1
Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
          5                   10                  15
Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
      20                  25                  30
Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
35                  40                  45

<210> 101
<211> 81
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -31..-1
<400> 101
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
    -30                 -25                 -20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15                  -10                 -5                  1
Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
              5                   10                  15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
          20                  25                  30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
      35                  40                  45
Leu
50

<210> 102
```

<211> 126
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -20..-1
<400> 102

```
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
-20                 -15                 -10                  -5
Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
                    1                   5                   10
Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
            15                  20                  25
Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
        30                  35                  40
Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
45                  50                  55                  60
Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
                    65                  70                  75
Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
                80                  85                  90
Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
            95                  100                 105
```

<210> 103
<211> 273
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -45..-1
<220>
<221> UNSURE
<222> 181,187,193,196,198,199,203,212,214
<223> Xaa = any one of the twenty amino acids
<400> 103

```
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
-45                 -40                 -35                  -30
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
                    -25                 -20                 -15
Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
                -10                 -5                  1
Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
    5                   10                  15
Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
20                  25                  30                  35
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
                    40                  45                  50
Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
                55                  60                  65
Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
            70                  75                  80
Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
        85                  90                  95
Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
100                 105                 110                 115
Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
                120                 125                 130
```

```
Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
            135                 140                 145
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
        150                 155                 160
Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
    165                 170                 175
Met Xaa Thr Gly His His Pro Xaa Asp Thr Thr Phe Ser Xaa Lys Gln
180                 185                 190                 195
Xaa Asp Xaa Xaa Ser Gly Asp Xaa Ile Phe Leu Gly Ser Asp Ser His
                200                 205                 210
Xaa Pro Xaa Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
            215                 220                 225
Leu
```

<210> 104
<211> 158
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -37..-1
<400> 104

```
Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro
        -35                 -30                 -25
Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His
    -20                 -15                 -10
Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr
-5                  1                   5                   10
Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser
            15                  20                  25
Phe Glu His Leu Gln Ala Asn Gln His Arg Ala Asn Ile Val Glu Arg
        30                  35                  40
Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu
    45                  50                  55
Cys Asp His His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg
60                  65                  70                  75
Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His
                80                  85                  90
His Thr Gly Pro His Gly Gly Ser Ile Gln Gly Met Ser Gly Glu Thr
            95                  100                 105
Pro Gly Ser Pro Gln Glu Ala Glu Glu Gly Arg Gly Gly Ser
        110                 115                 120
```

<210> 105
<211> 51
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -19..-1
<220>
<221> UNSURE
<222> 8
<223> Xaa = any one of the twenty amino acids
<400> 105

```
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
                -15                 -10                 -5
Val His Thr Thr Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Gln Arg
```

```
            1               5                   10
Arg Cys Trp Arg Arg Val Ser Phe Gln Ile Ser Arg Cys Lys Thr Gly
    15                  20                  25
Val Trp Trp
30

<210> 106
<211> 359
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -34..-1
<220>
<221> UNSURE
<222> 20,64,65,130,156,282,288,289,294,296,300,302,310
<223> Xaa = any one of the twenty amino acids
<400> 106
Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
                -30                 -25                 -20
Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
            -15                 -10                 -5
Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
        1                   5                   10
Asp Asp Leu Pro Ala Xaa Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
15                  20                  25                  30
Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
                35                  40                  45
Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
            50                  55                  60
Ile Xaa Xaa Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
        65                  70                  75
Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp
    80                  85                  90
Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp
95                  100                 105                 110
Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp
                115                 120                 125
Glu Phe Thr Xaa Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe
            130                 135                 140
Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Xaa Val Gly
        145                 150                 155
Ile Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Leu Ser Arg
    160                 165                 170
Asp Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys
175                 180                 185                 190
Lys Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys
                195                 200                 205
Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu
            210                 215                 220
Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr
        225                 230                 235
Lys Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser
    240                 245                 250
Gln Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu
255                 260                 265                 270
Val Thr Glu His Thr Pro Leu Leu Arg Pro Leu Xaa Phe Cys Gln Cys
                275                 280                 285
```

Pro Xaa Xaa Phe Gly Ala Leu Xaa Gly Xaa Pro Ala His Xaa Gln Xaa
290 295 300
His Asp Arg Ile Ile Gln Thr Xaa Glu Glu Asp Asp Asn Glu Asp Thr
305 310 315
Asp Ser Ser Asp Ala Glu Glu
320 325

<210> 107
<211> 291
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 107
Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
-40 -35 -30
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
-25 -20 -15
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
-10 -5 1 5
Met Cys Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg
10 15 20
Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu
25 30 35
Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val
40 45 50
Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr
55 60 65 70
Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser
75 80 85
Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala
90 95 100
Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile
105 110 115
Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp
120 125 130
Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys
135 140 145 150
Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
155 160 165
Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
170 175 180
Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
185 190 195
Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
200 205 210
Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
215 220 225 230
Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
235 240 245
Asn Lys Ala

<210> 108
<211> 67
<212> PRT
<213> Homo sapiens
<220>

```
<221> SIGNAL
<222> -26..-1
<400> 108
Met Ser Thr Trp Leu Leu Leu Ile Ala Leu Lys Thr Leu Ile Thr Trp
    -25                 -20                 -15
Val Ser Leu Phe Ile Asp Cys Val Met Thr Arg Lys Leu Thr Asn Cys
-10                 -5                  1               5
Asn Ala Arg Glu Thr Ile Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn
            10                  15                  20
Cys Phe Ala Ile Arg His Phe Glu Asn Lys Phe Ala Val Glu Thr Leu
        25                  30                  35
Ile Cys Ser
    40

<210> 109
<211> 127
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -63..-1
<400> 109
Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
            -60                 -55                 -50
Leu Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
        -45                 -40                 -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
    -30                 -25                 -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
-15                 -10                 -5                      1
Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
            5                   10                  15
Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu
        20                  25                  30
Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe
    35                  40                  45
Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys
50                  55                  60

<210> 110
<211> 97
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -20..-1
<220>
<221> UNSURE
<222> 53
<223> Xaa = any one of the twenty amino acids
<400> 110
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20                 -15                 -10                     -5
Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys Gly Ala Cys Arg
                1               5                   10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
        15                  20                  25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
```

```
    30                  35                  40
Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys Thr Lys Val Ala
45                  50                  55                  60
His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys Lys Gly Pro Trp
                65                  70                  75
Ser

<210> 111
<211> 86
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -20..-1
<400> 111
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20                 -15                 -10                 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
                1                   5                   10
Ala Leu Val Asp Glu Thr Arg Met Gly Asn Cys Pro Gly Gly Pro Gln
        15                  20                  25
Glu Asp His Ser Asp Gly Ile Phe Pro Asp Gln Ser Arg Trp Gln Pro
    30                  35                  40
Val Ser Gly Gly Gly Ala Leu Cys Pro Leu Arg Gly Pro Pro His Arg
45                  50                  55                  60
Ala Ala Gly Gly Asp Met
                65

<210> 112
<211> 71
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -25..-1
<400> 112
Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25                 -20                 -15                 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
                -5                  1                   5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
        10                  15                  20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
    25                  30                  35
Ser Gln Gln Glu Glu Leu Lys
40                  45

<210> 113
<211> 60
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 113
Met Asp Gly His Trp Ser Ala Ala Phe Ser Ala Leu Thr Val Thr Ala
        -40                 -35                 -30
Met Ser Ser Trp Ala Arg Arg Arg Ser Ser Ser Ser Arg Arg Ile Pro
```

```
    -25                 -20                 -15
Ser Leu Pro Gly Ser Pro Val Cys Trp Ala Trp Pro Trp Tyr Pro Asp
-10                 -5                  1                   5
Thr Thr Ser Phe Pro Leu Arg Cys Arg Gly Arg Val
            10                  15

<210> 114
<211> 118
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -83..-1
<220>
<221> UNSURE
<222> 28,32
<223> Xaa = any one of the twenty amino acids
<400> 114
Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala Gln Ala Gly Val Gln
            -80                 -75                 -70
Trp Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu Phe Lys Gly
        -65                 -60                 -55
Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro
    -50                 -45                 -40
Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr Gly Leu His
-35                 -30                 -25                 -20
His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys Ser Pro Pro
                -15                 -10                 -5
Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser His Val Pro
            1                   5                   10
Gly Lys Lys Lys Leu Leu Lys Val Glu Lys Lys Asn Leu Arg Xaa Leu
    15                  20                  25
Leu Thr Xaa Ile Lys Thr
30                  35

<210> 115
<211> 76
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<220>
<221> UNSURE
<222> 22,43
<223> Xaa = any one of the twenty amino acids
<400> 115
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
        -20                 -15                 -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
    -5                  1                   5                   10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Xaa Phe Gly Lys Ala
                15                  20                  25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
            30                  35                  40
Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
        45                  50
```

<210> 116
<211> 95
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -52..-1
<400> 116
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
-50 -45 -40
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
-35 -30 -25
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
-20 -15 -10 -5
Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
1 5 10
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
15 20 25
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
30 35 40

<210> 117
<211> 82
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 117
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
-20 -15 -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
-5 1 5 10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
15 20 25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
30 35 40
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Gly
45 50 55
Arg Asn
60

<210> 118
<211> 89
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -16..-1
<400> 118
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
-15 -10 -5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
35 40 45

```
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
    50                  55                  60
Glu Ala Gly Ala Ser Leu Tyr Ser Pro
65                  70
```

<210> 119
<211> 30
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -19..-1
<400> 119

```
Met Thr Met Ala Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala
                -15                 -10                 -5
Leu Trp Ala Ala Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
            1               5                   10
```

<210> 120
<211> 115
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -103..-1
<400> 120

```
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
            -100                -95                 -90
Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
        -85                 -80                 -75
Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
    -70                 -65                 -60
Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
-55                 -50                 -45                 -40
Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
                -35                 -30                 -25
Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
            -20                 -15                 -10
Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg Cys Lys Gln Ser
        -5                  1               5
Ser Lys Pro
10
```

<210> 121
<211> 105
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -76..-1
<400> 121

```
Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr Leu Leu Leu Lys Trp
    -75                 -70                 -65
Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp Leu Val Ser Tyr Pro
-60                 -55                 -50                 -45
Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn Leu Asp Phe Pro Lys
                -40                 -35                 -30
Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr Arg Trp Phe Asn Leu
```

```
            -25                 -20                 -15
Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
        -10                 -5                  1
Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
5                   10                  15                  20
Glu Leu Arg Gln Val Val Glu Val Ser
                25
```

<210> 122
<211> 93
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 122

```
Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
        -20                 -15                 -10
Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
    -5                  1                   5                   10
Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
                15                  20                  25
Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
            30                  35                  40
Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
        45                  50                  55
Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
    60                  65                  70
```

<210> 123
<211> 109
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 123

```
Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
        -40                 -35                 -30
Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
    -25                 -20                 -15
Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Ile Ile
-10                 -5                  1                   5
Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
            10                  15                  20
Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
        25                  30                  35
Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met
    40                  45                  50
Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Gly Val
55                  60                  65
```

<210> 124
<211> 51
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL

<222> -15..-1
<400> 124
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15 -10 -5 1
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
5 10 15
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
20 25 30
Met Leu Val
35

<210> 125
<211> 56
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -27..-1
<400> 125
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 1 5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
10 15 20
Trp Cys Ile Gln Pro Trp Ala Lys
25

<210> 126
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -21..-1
<400> 126
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
-20 -15 -10
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
-5 1 5 10
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
15 20 25
Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser
30 35 40
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
45 50 55
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
60 65 70 75
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
80 85 90
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
95 100 105
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
110 115 120
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
125 130 135
Arg Arg
140

<210> 127
<211> 126
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -68..-1
<400> 127
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
-65 -60 -55
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
-50 -45 -40
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
-35 -30 -25
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20 -15 -10 -5
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
1 5 10
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
15 20 25
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
30 35 40
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala
45 50 55

<210> 128
<211> 140
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -40..-1
<400> 128
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40 -35 -30 -25
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20 -15 -10
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
-5 1 5
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10 15 20
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25 30 35 40
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45 50 55
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60 65 70
Leu Ala Phe Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu
75 80 85
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90 95 100

<210> 129
<211> 43
<212> PRT
<213> Homo sapiens
<220>

<221> SIGNAL
<222> -24..-1
<400> 129
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-20 -15 -10
Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
-5 1 5
Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
10 15

<210> 130
<211> 69
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -21..-1
<400> 130
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
15 20 25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
30 35 40
Val Leu Cys Gln Lys
45

<210> 131
<211> 78
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -19..-1
<400> 131
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
-15 -10 -5
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
1 5 10
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15 20 25
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val
30 35 40 45
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
50 55

<210> 132
<211> 80
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -47..-1
<400> 132
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
-45 -40 -35

```
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
    -30                 -25                 -20
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
-15                 -10                 -5                  1
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
            5                   10                  15
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
        20                  25                  30
```

<210> 133
<211> 53
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 133

```
Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
        -40                 -35                 -30
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
    -25                 -20                 -15
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
-10                 -5                  1                   5
Met Cys Leu Lys Ile
            10
```

<210> 134
<211> 1053
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 131..169
<223> Von Heijne matrix
score 4.19999980926514
seq MLAVSLTVPLLGA/MM
<220>
<221> polyA_site
<222> 1042..1053
<400> 134

```
gagcgagtcg gacgggctgc gacagcgccg gcccctgcgg ccgcaggtcg tcacagacga     60
tgatggccag gccccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt    120
gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc        169
           Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
                       -10                 -5
atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa      217
Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
1               5                   10                  15
gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga      265
Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
            20                  25                  30
cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata      313
Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
        35                  40                  45
gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc      361
Ala His Ile Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val
    50                  55                  60
gta aaa ctt gaa aat ggt gaa ata gag acc att gcc cgg ttt ggt tcg      409
```

```
Val Lys Leu Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser
65                  70                  75                  80
ggc cct tgc aaa acc cga ggt gat gag cct gtg tgt ggg aga ccc ctg      457
Gly Pro Cys Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu
                85                  90                  95
ggt atc cgt gca ggg ccc aat ggg act ctc ttt gtg gcc gat gca tac      505
Gly Ile Arg Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr
            100                 105                 110
aag gga cta ttt gaa gta aat ccc tgg aaa cgt gaa gtg aaa ctg ctg      553
Lys Gly Leu Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu
        115                 120                 125
ctg tcc tcc gag aca ccc att gag ggg aag aac atg tcc ttt gtg aat      601
Leu Ser Ser Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn
    130                 135                 140
gat ctt aca gtc act cag gat ggg agg aag att tat ttc acc gat tct      649
Asp Leu Thr Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser
145                 150                 155                 160
agc agc aaa tgg caa aga cga gac tac ctg ctt ctg gtg atg gag ggc      697
Ser Ser Lys Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly
                165                 170                 175
aca gat gac ggg cgc ctg ctg gag tat gat act gtg acc agg gaa gta      745
Thr Asp Asp Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val
            180                 185                 190
aaa gtt tta ttg gac cag ctg cgg ttc ccg aat gga gtc cag ctg tct      793
Lys Val Leu Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser
        195                 200                 205
cct gca gaa gac ttt gtc ctg gtg gca gaa aca acc atg gcc agg ata      841
Pro Ala Glu Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile
    210                 215                 220
cga aga gtc tac gtt tct ggc ctg atg aag ggc ggg gct gat ctg ttt      889
Arg Arg Val Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe
225                 230                 235                 240
gtg gag aac atg cct gga ttt cca gac aac atc cgg ccc agc agc tct      937
Val Glu Asn Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser
                245                 250                 255
ggg ggg tac tgg gtg ggc atg tcg acc atc cgc cct aac cct ggg ttt      985
Gly Gly Tyr Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe
            260                 265                 270
tcc atg ctg gat ttc tta tct gag aga ccc tgg att aaa agg atg att     1033
Ser Met Leu Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile
        275                 280                 285
ttt aag gta aaaaaaaaaa a                                         1053
Phe Lys Val
    290
```

<210> 135
<211> 675
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 638..643
<220>
<221> polyA_site
<222> 662..675
<400> 135

```
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      60
gtagcagtgg ttcagcacac tttggtatgt tgactgtta atg atg tac gtt tct        114
```

```
                                                Met Met Tyr Val Ser
                                                1               5
ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc      162
Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
                10                  15                  20
tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa      210
Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
            25                  30                  35
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      258
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
        40                  45                  50
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatggtttat             306
Tyr Val Cys Val Phe Ile
    55
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca    366
tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga    426
tatttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg    486
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt    546
cagagaagaa catttaaagg gttaatattt ttgaaacgtt ttcagataat atctatttga    606
ttattgtggc ttctatttga aatgtgtcta aaataaatgc tgtttattta aaatgaaaaa    666
aaaaaaaaa                                                           675

<210> 136
<211> 1112
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 111..194
<223> Von Heijne matrix
      score 4.80000019073486
      seq GVLLEPFVHQVGG/HS
<220>
<221> polyA_signal
<222> 1080..1085
<220>
<221> polyA_site
<222> 1101..1112
<400> 136
ccgagagaga ctacacggta ctgggacaca cggacaaaca acagacagaa gacgtactgg     60
ccgctggact ccgctgcctc ccccatctcc ccgccatctg cgcccggagg atg agc       116
                                                          Met Ser
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt      164
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
    -25                 -20                 -15
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc      212
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
-10                 -5                  1               5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag      260
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
            10                  15                  20
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac      308
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr
        25                  30                  35
aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat      356
Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu Pro His
    40                  45                  50
ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag gga agt gtg gcc          401
```

```
Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val Ala
55                  60                  65
tgaatacccc accccggctc ctctgcaccc agagctgggg gccacctcag aagtgtcatc    461
tctctctgag cacgcattcc cctgcagcag tcgaggactg agcagattga gtgatgctgg    521
ggcagagagg cctgagagga aaggtgttca gccagtcgtt tgtaaggcgc tcgtcggcac    581
ctgctgaaac gcccccacct gacagcccca tcctcaaaga ctgtcttaat tactcatggc    641
aggttctaga gacttaaggg gaaaagctgc tttcaaggcc accacatgtc tgtgctcccc    701
aaccagctct atctgccttg tgttcatttt gttattttgt gacgtgagac agcaaagacc    761
aataaaaaca tattttataa gaacaaaagg cctgggtgcc tacccgtgtg ggggcactgt    821
gggaagcctt tgctagggtg tcttgtgctg tgtggtttgt tttgtttgcc cctttatttt    881
gctttgctta cccagtcttc ccttactctt ggatgcttct taaccctcag gcaaacctgt    941
gttccccctg tattcaggct ctgctttaaa gcaagccatg aggctgttgg agtttctgtt   1001
tagggcatta aaaattcccg caaactataa agagcaatgt tttcagtctt ttaggattag   1061
aagaattaca taaaaattaa taaacatttt caatgatgga aaaaaaaaaa a             1112

<210> 137
<211> 547
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 359..454
<223> Von Heijne matrix
      score 4
      seq FSFMLLGMGGCLP/GF
<220>
<221> polyA_site
<222> 536..547
<400> 137
ctggggagcc ctgcctaaga ctcatgctac aagaagttaa ataagtttcc cgaagtcaca     60
cagctagcct ctcatccctt ttctactgag aggaagtgga atgcactccg acaaggataa    120
ggttttattg tgagctggcc ttggaattaa accaccacca acacactttt ggattatcag    180
aaggtggaag gagtgcaaaa atgtcattcc catgcttgtc tgccaggcaa cctggtgtcc    240
attctttatg acgcctttcc tgaatcacag gtgcattggg gtgcttcctc ctccccagga    300
ctcccaccca actttgtgaa cacaacccac ttagaggagt tatctcagca cattatga      358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct      406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
       -30                 -25                 -20
ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct      454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
    -15                 -10                 -5
gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc      502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1               5                   10                  15
acc ttt gcc cat taaagtcaat tctccaccca taaaaaaaaa aaa                 547
Thr Phe Ala His
            20

<210> 138
<211> 1198
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 26..316
<223> Von Heijne matrix
      score 4
      seq RLPLVVSFIASSS/AN
```

<220>
<221> polyA_signal
<222> 1164..1169
<220>
<221> polyA_site
<222> 1187..1198
<400> 138

```
atcctgcgaa agaagggggt tcatc atg gcg gat gac cta aag cga ttc ttg        52
                            Met Ala Asp Asp Leu Lys Arg Phe Leu
                                -95                 -90
tat aaa aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca       100
Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser
            -85                 -80                 -75
gat aga gat gga gta cct gtt gtt aaa gtg gca aat gac aat gct cca       148
Asp Arg Asp Gly Val Pro Val Val Lys Val Ala Asn Asp Asn Ala Pro
        -70                 -65                 -60
gag cat gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca       196
Glu His Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr
    -55                 -50                 -45
gac caa gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt       244
Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys
-40                 -35                 -30                 -25
tac tat aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg       292
Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val
                -20                 -15                 -10
gtg agt ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc       340
Val Ser Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser
            -5                  1                   5
cta gaa aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg       388
Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val
    10                  15                  20
gaa gtt tct taatctgaca gtggtttcag tgtgtacctt atcttcatta               437
Glu Val Ser
25
taacaacaca atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct     497
caagaaaggg ccccttttc caacttatac taaagagcta gcatatagat gtaatttata     557
gatagatcag ttgctatatt ttctggtgta gggtctttct tatttagtga gatctaggga     617
taccacagaa atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat     677
ggatgagaga ttctattcag tggattagaa tcaaactggt acattgatcc acttgagccg     737
ttaagtgctg ccaattgtac aatatgccca ggcttgcaga ataaagccaa ctttttattg     797
tgaataataa taaggacata tttttcttca gattatgttt tatttctttg cattgagtga     857
ggtacataaa atggcttggt aaaagtaata aaatcagtac aatcactaac tttcctttgt     917
acatattatt ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg     977
ctgctcttta atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg    1037
taaccaatca gtgttttaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat    1097
tctgtttcca atgttagtat gtatgtaaac atgatagtac agccattttt ttcatatgtg    1157
agtaaaaata aaatagtatt tttaaaagta aaaaaaaaaa a                       1198
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<210> 139
<211> 1400
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 36..107
<223> Von Heijne matrix
score 5.69999980926514
seq ILGLLGLLGTLVA/ML

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<220>
<221> polyA_signal
<222> 1302..1307
<220>
<221> polyA_site
<222> 1389..1400
<400> 139
cagtccctga agacgcttct actgagaggt ctgcc atg gcc tct ctt ggc ctc          53
                                      Met Ala Ser Leu Gly Leu
                                                      -20
caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca ctg        101
Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr Leu
            -15                 -10                 -5
gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt gcc        149
Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly Ala
        1               5                   10
agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa tgt        197
Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu Cys
15                  20                  25                  30
gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc ctt        245
Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu
                35                  40                  45
ctg ggc ctg ccc gct gac atc cag gct gcc cag gcc atg atg gtg aca        293
Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr
            50                  55                  60
tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc atg        341
Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met
        65                  70                  75
aga tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg gcg        389
Arg Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala
    80                  85                  90
gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc att        437
Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile
95                  100                 105                 110
cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca cca        485
Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
                115                 120                 125
ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac ttg        533
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr Leu
            130                 135                 140
ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc tgc        581
Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu Cys
        145                 150                 155
ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc tac        629
Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala Tyr
    160                 165                 170
caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa cct        677
Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln Pro
175                 180                 185                 190
ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat gtg        725
Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr Val
                195                 200                 205
tgaagaacca ggggccagag ctgggggggtg gctgggtctg tgaaaaacag tggacagcac    785
cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaaggtg ctgctgaggg    845
tagactgact ttggccattg gattgagcaa aggcagaaat gggggctagt gtaacagcat    905
gcaggttgaa ttgccaagga tgctcgccat gccagccttt ctgttttcct caccttgctg    965
ctcccctgcc ctaagtcccc aaccctcaac ttgaaacccc attcccttaa gccaggactc   1025
agaggatccc tttgccctct ggtttacctg ggactccatc cccaaaccca ctaatcacat   1085
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cccactgact gaccctctgt gatcaaagac cctccctctg gctgaggttg gctcttagct   1145
cattgctggg gatgggaagg agaagcagtg gcttttgtgg gcattgctct aacctacttc   1205
tcaagcttcc ctccaaagaa actgattggc cctggaacct ccatcccact cttgttatga   1265
ctccacagtg tccagactaa tttgtgcatg aactgaaata aaaccatcct acggtatcca   1325
gggaacagaa agcaggatgc aggatgggag gacaggaagg cagcctggga catttaaaaa   1385
aataaaaaaa aaaaa                                                    1400

<210> 140
<211> 538
<212> DNA
<213> Homo sapiens
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<222> 35..130
<223> Von Heijne matrix
      score 8
      seq VPMLLLIAGGSFG/LR
<220>
<221> polyA_signal
<222> 505..510
<220>
<221> polyA_site
<222> 526..538
<400> 140
gcttggagtt ctgagccgat ggaggagttc actc atg ttt gca ctc gcg gtg atg     55
                                      Met Phe Ala Leu Ala Val Met
                                                      -30
cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg      103
Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu
-25                 -20                 -15                 -10
ttg ctg att gct gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc      151
Leu Leu Ile Ala Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile
               -5                  1               5
cga tat gat gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa      199
Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys
        10                  15                  20
ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag gga agt atc      247
Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Gly Ser Ile
    25                  30                  35
tgt tgaagggcta ctatctttcc ttggcccttc tcccttgttg ggactcaatc          300
Cys
40
tccagactat ctccccagag aatcttgtca aggcttggct ttaagctttg ttgggaaaat   360
caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt gggaagatcc   420
tgacctcctc caaggaagaa atccagaaag ccttaagact aagacaactt gactctgctg   480
attcttttt ccttttttt tttaaataaa aatactatta actggaaaaa aaaaaaaa       538

<210> 141
<211> 1167
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 169..267
<223> Von Heijne matrix
      score 7.80000019073486
      seq LTFLFLHLPPSTS/LF
<220>
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<221> polyA_signal
<222> 1132..1137
<220>
<221> polyA_site
<222> 1155..1167
<400> 141
gtaggaacta ctgtcccaga gctgaggcaa ggggatttct caggtcattt ggagaacaag      60
tgctttagta gtagtttaaa gtagtaactg ctactgtatt tagtggggtg gaattcagaa     120
gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag      177
                                                     Met Ser Gln
aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct       225
Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser
-30                 -25                 -20                 -15
gcc ctt aca ttt ttg ttt ctc cat cta cca cca tcc acc agt cta ttt       273
Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe
                -10                 -5                  1
att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg       321
Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu
        5                   10                  15
ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc       369
Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser
    20                  25                  30
tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa       417
Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys
35                  40                  45                  50
aga aaa aca aaa tgc taatgaagcc atcagtcaag ggtcacatgc caataaacaa       472
Arg Lys Thr Lys Cys
                55
taaattttcc agaagaaatg aaatccaact agacaaataa agtagagctt atgaaatggt     532
tcagtaagga tgagcttgtt gtttttgtt ttgttttgtt ttgtttttt aaagacggag       592
tctcgctctg tcactcaggc tggagtgcag tggtatgatc ttggctcact gtaacctccg     652
cctcccgggt tcaagccatt ctcctgcctc agtctcctga gtagctggga ttgcaggtgc     712
gtgccaccat gcctggctaa tttttgtgtt tttggtagag acagggtttc accacgttgg     772
tcgggctggt ctcgggctcc tgacctcttg atccgcctgc cttggcctcc caaagtgatg     832
ggattacaga tgtgagccac cgtgcctagc caaggatgag atttttaaag tatgttccag     892
ttctgtgtca tggttggaag acagagtagg aaggatatgg aaaaggtcat ggggaagcag     952
aggtgattca tggctctgtg aatttgaggt gaatggttcc ttattgtcta ggccacttgt    1012
gaagaatatg agtcagttat tgccagcctt ggaatttact tctctagctt acaatggacc    1072
ttttgaactg ggaaacacct tgtctgcatt cactttaaaa tgtcaaaact aatttttata    1132
ataaatgttt attttcacat cgaaaaaaaa aaaaa                               1167

<210> 142
<211> 730
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 143..238
<223> Von Heijne matrix
      score 8.80000019073486
      seq VPMLLLIVGGSFG/LR
<220>
<221> polyA_signal
<222> 697..702
<220>
<221> polyA_site
<222> 721..730
<220>
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<221> misc_feature
<222> 1,14,28,52
<223> n=a, g, c or t
<400> 142
nctttgcctt tctntccaca ggtgtccnct cccaggtcca actgcagact tngaattcgt     60
cttggtgaga gcgtgagctg ctgagatttg ggagtctgcg ctaggcccgc ttggagttct    120
gagccgatgg aagagttcac tc atg ttt gca ccc gcg gtg acg cgt gct ttt     172
                         Met Phe Ala Pro Ala Val Thr Arg Ala Phe
                            -30                 -25
cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att      220
Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile
        -20                 -15                 -10
gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat      268
Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp
    -5                  1               5                   10
gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag      316
Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu
                15                  20                  25
aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag      364
Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys
            30                  35                  40
ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct      412
Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro
        45                  50                  55
gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act      460
Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
    60                  65                  70
tgactctgct gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt    520
cctaatatat acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg    580
ggtaatttga tgacaaataa tcttcactaa aggtcatgta caggttttta tacttcccag    640
ctattccatc tgtggatgaa agtaacaatg ttggccacgt atattttaca cctcgaaata    700
aaaaatgtga atactgctcc aaaaaaaaaa                                     730

<210> 143
<211> 1174
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 108..170
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTSA/AF
<220>
<221> polyA_signal
<222> 1141..1146
<220>
<221> polyA_site
<222> 1161..1174
<400> 143
cacgttcctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc     60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg      116
                                                Met Trp Trp
                                                   -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
            -15                 -10                 -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212
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Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
        1               5                  10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca      260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15                  20                  25                  30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgc      308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
                35                  40                  45
att gct acc att tat gtt cgt tat aag caa gtt cat gct ctg agt cct      356
Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala Leu Ser Pro
            50                  55                  60
gaa gag aac gtt atc atc aaa tta aac aag gct ggc ctt gta ctt gga      404
Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu Val Leu Gly
        65                  70                  75
ata ctg agt tgt tta gga ctt tct att gtg gca aac ttc cag aaa aca      452
Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe Gln Lys Thr
    80                  85                  90
acc ctt ttt gct gca cat gta agt gga gct gtg ctt acc ttt ggt atg      500
Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr Phe Gly Met
95                  100                 105                 110
ggc tca tta tat atg ttt gtt cag acc atc ctt tcc tac caa atg cag      548
Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln
                115                 120                 125
ccc aaa atc cat ggc aaa caa gtc ttc tgg atc aga ctg ttg ttg gtt      596
Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Leu Val
            130                 135                 140
atc tgg tgt gga gta agt gca ctt agc atg ctg act tgc tca tca gtt      644
Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val
        145                 150                 155
ttg cac agt ggc aat ttt ggg act gat tta gaa cag aaa ctc cat tgg      692
Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
    160                 165                 170
aac ccc gag gac aaa ggt tat gcg ctt cac atg atc act act gca gca      740
Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr Thr Ala Ala
175                 180                 185                 190
gaa tgg tct atg tca ttt tcc ttc ttt ggt ttt ttc ctg act tac att      788
Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile
                195                 200                 205
cgt gat ttt cag aaa att tcc tta cgg gtg gaa gcc aac tta cat gga      836
Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn Leu His Gly
            210                 215                 220
tta acc ctc tat gac act gca cct tgc cct att aac aat gaa cga aca      884
Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn Glu Arg Thr
        225                 230                 235
cgg cta ctt tcc aga gat att aga tgaaaggata aaatatttct gtaatgatta      938
Arg Leu Leu Ser Arg Asp Ile Arg
    240                 245
tgattctcag ggattgggga aaggttcaca gaagttgctt attcttctct gaaattttca     998
accacttaat caaggctgac agtaacactg atgaatgctg ataatcagga aacatgaaag    1058
aagccatttg atagattatt ctaaaggata tcatcaagaa gactattaaa aacacctatg    1118
cctatacttt tttatctcag aaaataaagt caaaagacta tgaaaaaaaa aaaaaa        1174

<210> 144
<211> 1158
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
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<222> 1133..1138
<220>
<221> polyA_site
<222> 1146..1158
<220>
<221> misc_feature
<222> 652
<223> n=a, g, c or t
<400> 144

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aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc     60
tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcatcctgs    120
tgrsagtgta mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct    180
aacagtccat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca       232
                               Met Gly Cys Val Phe Gln Ser Thr
                               1               5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
    10                  15                  20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
25                  30                  35                  40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
                45                  50                  55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
            60                  65                  70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
        75                  80                  85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
    90                  95                  100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag          572
Gln Met Leu Thr
105
gcaaggaaac tgattatctt gagtaaatgc cagcctttgg gctaagtact taccacagag    632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat    692
tttagttaak aataaaatat tgataattat tgtattatta ctttaaacac acttcccccc    752
cacaaaagcc ctgtgaagga tgttttgttc acatataatg tccaaatatg ttttggacac    812
atatttatta aatggaataa atagtamttg aaccctggca ccthtgacaa caaagtcyat    872
gttyttttta ctatgcccta ataccttttsa tcagttatcc acattgatgc tacatytgta    932
ttttataggt accctatgtt aggtgttttg ggggatagaa aagaaataag cagkycaggc    992
tcagtggctc atgcctgtaa tcctagcatt ttgggaggct gaggcagcag aamtgcctga   1052
gccccagggt tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwga   1112
cagagcaaga ctytgtttaa aataaaaaaa gagaaaaaaa aaaaaa                  1158
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<210> 145
<211> 754
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 5..142
<223> Von Heijne matrix
score 6.59999990463257
seq VCCYLFWLIAILA/QL
<220>

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<221> polyA_signal
<222> 716..721
<220>
<221> polyA_site
<222> 742..754
<400> 145
tgtg atg agc gtg ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc      49
     Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
         -45                 -40                 -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
    -30                 -25                 -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa     145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
-15                 -10                 -5                  1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat     193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
            5                   10                  15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgctca            241
Leu Lys Tyr His Trp Pro
        20
gtctttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc    301
acttttcttg acttgcctgt tttggccatt agctgcctta aacgttaaca gcacatttga    361
atgccttatt ctacaatgca gcgtgttttc ctttgccttt tttgcacttt ggtgaattac    421
gtgcctccat aacctgaact gtgccgactc cacaaaacga ttatgtactc ttctgagata    481
gaagatgctg ttcttctgag agatacgtta ctctctcctt ggaatctgtg gatttgaaga    541
tggctcctgc cttctcacgt gggaatcagt gaagtgttta gaaactgctg caagacaaac    601
aagactccag tggggtggtc agtaggagag cacgttcaga gggaagagcc atctcaacag    661
aatcgcacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa    721
tattttcctc ctttctatgt aaaaaaaaaa aaa                                 754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 98..181
<223> Von Heijne matrix
      score 3.59999990463257
      seq PLSDSWALLPASA/GV
<220>
<221> polyA_signal
<222> 1035..1040
<220>
<221> polyA_site
<222> 1060..1073
<400> 146
ccgattacag ctaggtagtg gagcgccgct gcttacctgg gtgcaggaga cagccggagt     60
cgctgggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct     115
                                        Met Trp Arg Leu Leu Ala
                                                -25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca      163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
        -20                 -15                 -10
ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt      211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser
    -5                  1               5                   10
```

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ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa      259
Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu
                15                  20                  25
agg gca cca ctt gtg cca aaa gta aga aga gaa cct aaa aat tta agt      307
Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser
            30                  35                  40
gac ata cgg gga cct tcc act gaa gct acg gag ttt aca gaa ggc aat      355
Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu Phe Thr Glu Gly Asn
        45                  50                  55
ttt gca atc ttg gca ttg ggt ggt ggc tac ctg cat tgg ggc cac ttt      403
Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe
    60                  65                  70
gaa atg atg cgc ctg aca atc aac cgc tct atg gac ccc aag aac atg      451
Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met
75                  80                  85                  90
ttt gcc ata tgg cga gta cca gcc cct ttc aag ccc atc act cgc aaa      499
Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys
                95                  100                 105
agt gtt ggg cat cgc atg ggg gga ggc aaa ggt gct att gac cac tac      547
Ser Val Gly His Arg Met Gly Gly Gly Lys Gly Ala Ile Asp His Tyr
            110                 115                 120
gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt      595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg
        125                 130                 135
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag      643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys
    140                 145                 150
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg      691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met
155                 160                 165                 170
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca      739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr
                175                 180                 185
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg      787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu
            190                 195                 200
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac      835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr
        205                 210                 215
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag      890
Met Pro Lys Arg Val
    220
aaggattctg catttctatt cccctcagcc tacccactga agtctttggg tagctcttaa    950
gccataacta aggagcagca tttgagtaga tttctgaaaa acgatgttat ttgttgattt   1010
aaaaagaaaa ctgtattttt attaaataaa atttaaacat cacttcagga aaaaaaaaaa   1070
aaa                                                                1073

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<213> Homo sapiens
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<222> 46..189
<223> Von Heijne matrix
      score 4.09999990463257
      seq VFMLIVSVLALIP/ET
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<222> 377..382
<220>
<221> polyA_site
<222> 402..413
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tgagaagagt tgagggaaag tgctgctgct gggtctgcag acgcg atg gat aac gtg 57
Met Asp Asn Val
-45
cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac 105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
-40 -35 -30
gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta 153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
-25 -20 -15
ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca 201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
-10 -5 1
ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc 249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5 10 15 20
ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc 297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
25 30 35
ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg 342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
40 45 50
taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca 402
aaaaaaaaaa a 413

<210> 148
<211> 609
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<213> Homo sapiens
<220>
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<222> 139..231
<223> Von Heijne matrix
score 4.40000009536743
seq TCCHLGLPHPVRA/PR
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<222> 579..584
<220>
<221> polyA_site
<222> 598..609
<400> 148
tgtcggagtt ggaaagggac gcctggtttc cccccaagcg aaccgggatg ggaagtgact 60
tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag 120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt 171
Met Ser Asn Thr His Thr Val Leu Val Ser Leu
-30 -25
ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac 219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20 -15 -10 -5
ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct 267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro
1 5 10

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agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc      315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe
        15                  20                  25
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg      363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser
    30                  35                  40
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta            411
Ala Asp Arg Cys Asp Leu
45                  50
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca    471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct    531
tcccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg    591
agctgcaaaa aaaaaaaa                                                  609

<210> 149
<211> 522
<212> DNA
<213> Homo sapiens
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<221> polyA_site
<222> 512..522
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<221> misc_feature
<222> 11
<223> n=a, g, c or t
<400> 149
ccaactgcag nttcgaattt accgagcgga gaggagatgc acacggcact cgagtgtgag     60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt     110
              Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys
              1               5                   10
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat      158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His
    15                  20                  25
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa      206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu
30                  35                  40                  45
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa      254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys
                50                  55                  60
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta      302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu
            65                  70                  75
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag      350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu
        80                  85                  90
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt      398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val
    95                  100                 105
tct cat tta ggt att ttg gca gtt caa gag gga aag cat ttt cac tca      446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser
110                 115                 120                 125
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act      494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr
                130                 135                 140
gtg acc agt gta tcc aca aaaaaaaaaa                                   522
Val Thr Ser Val Ser Thr
            145
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<210> 150
<211> 1322
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 126..260
<223> Von Heijne matrix
score 4.59999990463257
seq VLVYLVTAERVWS/DD
<220>
<221> polyA_signal
<222> 1283..1288
<220>
<221> polyA_site
<222> 1309..1322
<400> 150

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ccgaaaacct tccccgcttc tggatatgaa attcaagctg cttgctgagt cctattgccg      60
gctgctggga gccaggagag ccctgaggag tagtcactca gtagcagctg acgcgtgggt     120
ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag     170
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys
      -45                 -40                 -35
tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc      218
Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe
-30                 -25                 -20                 -15
cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac      266
Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp
                -10                 -5                  1
cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc      314
His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val
        5                   10                  15
tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg      362
Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu
    20                  25                  30
cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg      410
Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val
35                  40                  45                  50
gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag      458
Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu
                55                  60                  65
aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc      506
Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu
            70                  75                  80
tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc      554
Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile
        85                  90                  95
gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct      602
Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro
    100                 105                 110
cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc      650
Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys
115                 120                 125                 130
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg      698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val
                135                 140                 145
gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac      746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr
            150                 155                 160
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ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa      794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln
        165                 170                 175
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa      842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys
    180                 185                 190
caa gac gac ctc ctt tcg ggt gac ctc atc ttt ctg ggc tca gac agt      890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser
195                 200                 205                 210
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc      938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr
                215                 220                 225
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct      994
Ile Leu
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag   1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct   1114
gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg tttccttttc   1174
tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg ttcatagaag   1234
aacacacatg cgggcacctt catcgtgtgt ggcccactgt cagaacttaa taaaagtcaa   1294
ctcatttgct ggttaaaaaa aaaaaaaa                                      1322

<210> 151
<211> 1290
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 50..160
<223> Von Heijne matrix
      score 4
      seq PLSLDCGHSLCRA/CI
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<221> polyA_site
<222> 1280..1290
<400> 151
gaggagagcc tcaggagtta ggaccagaag aagccaggga agcagtgca atg gct tca     58
                                                  Met Ala Ser
                                                      -35
aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg      106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu
            -30                 -25                 -20
gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc      154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys
        -15                 -10                 -5
cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga      202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly
    1               5                   10
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat      250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His
15                  20                  25                  30
cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag      298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu
                35                  40                  45
gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat      346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys Asp His
            50                  55                  60
cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa gtc att      394
His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys Val Ile
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        65                  70                  75
tgc tgg ctt tgt gag cgg tct cag gag cac cgt ggt cac cac aca gtc      442
Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr Val
    80                  85                  90
ctc acg gag gaa gta ttc aag gaa tgt cag gag aaa ctc cag gca gtc      490
Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu Gln Ala Val
95                  100                 105                 110
ctc aag agg ctg aag aag gaa gag gag gaa gct gag aag ctg gaa gct      538
Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys Leu Glu Ala
                115                 120                 125
gac atc aga gaa gag aaa act tcc tgg aag tat cag gta caa act gag      586
Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val Gln Thr Glu
            130                 135                 140
aga caa agg ata caa aca gaa ttt gat cag ctt aga agc atc cta aat      634
Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser Ile Leu Asn
        145                 150                 155
aat gag gag cag aga gag ctg caa aga ttg gaa gaa gaa gaa aag aag      682
Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu Glu Lys Lys
    160                 165                 170
acg ctg gat aag ttt gca gag gct gag gat gag cta gtt cag cag aag      730
Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val Gln Gln Lys
175                 180                 185                 190
cag ttg gtg aga gag ctc atc tca gat gtg gag tgt cgg agt cag tgg      778
Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg Ser Gln Trp
                195                 200                 205
tca aca atg gag ctg ctg cag gac atg agt gga atc atg aaa tgg agt      826
Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met Lys Trp Ser
            210                 215                 220
gag atc tgg agg ctg aaa aag cca aaa atg gtt tcc aag aaa ctg aag      874
Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys Lys Leu Lys
        225                 230                 235
act gta ttc cat gct cca gat ctg agt agg atg ctg caa atg ttt aga      922
Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln Met Phe Arg
    240                 245                 250
gaa ctg aca gct gtc cgg tgc tac tgg gtg gat gtc aca ctg aat tca      970
Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr Leu Asn Ser
255                 260                 265                 270
gtc aac cta aat ttg aat ctt gtc ctt tca gaa gat cag aga caa gtg     1018
Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln Arg Gln Val
                275                 280                 285
ata tct gtg cca att tgg cct ttt cag tgt tat aat tat ggt gtc ttg     1066
Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr Gly Val Leu
            290                 295                 300
gga tcc caa tat ttc tcc tct ggg aaa cat tac tgg gaa gtg gac gtg     1114
Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu Val Asp Val
        305                 310                 315
tcc aag aaa act gcc tgg atc ctg ggg gta tac tgt aga aca tat tcc     1162
Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg Thr Tyr Ser
    320                 325                 330
cgc cat atg aag tat gtt gtt aga aga tgt gca aat cgt caa aat ctt     1210
Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg Gln Asn Leu
335                 340                 345                 350
tac acc aaa tac aga cct cta ttt ggc tac tgg gtt ata ggg tta cag     1258
Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile Gly Leu Gln
                355                 360                 365
aat aaa tgt aag tat ggt gcc aaaaaaaaaa a                           1290
Asn Lys Cys Lys Tyr Gly Ala
            370
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<210> 152
<211> 1364
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 83..139
<223> Von Heijne matrix
      score 8.60000038146973
      seq LLWLALACSPVHT/TL
<220>
<221> polyA_site
<222> 1356..1354
<400> 152
gcctgggagc tgaggcagcc accgtctcag cctggccagc cctctggacc ccgaggttgg      60
accctactgt gacacaccta cc atg cgg aca ctc ttc aac ctc ctc tgg ctt      112
                         Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
                                             -15                 -10
gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc      160
Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
                -5                  1                   5
aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat      208
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
        10                  15                  20
aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag      256
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
    25                  30                  35
agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac      304
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
40                  45                  50                  55
aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc      352
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
                60                  65                  70
cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc      400
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
            75                  80                  85
tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag      448
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
        90                  95                  100
gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg      496
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
    105                 110                 115
aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac      544
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
120                 125                 130                 135
tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata      592
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
                140                 145                 150
gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc      640
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
            155                 160                 165
gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc      688
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
        170                 175                 180
gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag      736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln
    185                 190                 195
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```
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg      784
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly
200                 205                 210                 215
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc      832
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala
                220                 225                 230
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg      880
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala
            235                 240                 245
cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc      928
His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val
        250                 255                 260
cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg      976
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly
    265                 270                 275
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag     1024
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu
280                 285                 290                 295
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc     1072
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro
                300                 305                 310
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag     1120
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
            315                 320                 325
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc     1168
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser
        330                 335                 340
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct     1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
    345                 350                 355
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc         1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
360                 365                 370
taggtgggca ttgcggcctc cgcggtggac gtgttctttt ctaagccatg gagtgagtga   1321
gcaggtgtga aatacaggcc tccactccgt ttgcaaaaaa aaa                      1364

<210> 153
<211> 1470
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 57..95
<223> Von Heijne matrix
      score 3.90000009536743
      seq MLLSIGMLMLSAT/QV
<220>
<221> polyA_signal
<222> 1438..1443
<220>
<221> polyA_site
<222> 1458..1470
<400> 153
gctggcaaga ctgtttgtgt tgcgggggcc ggacttcaag gtgattttac aacgag atg     59
                                                                 Met
ctg ctc tcc ata ggg atg ctc atg ctg tca gcc aca caa gtc tac acc      107
Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr
        -10                 -5                  1
```

```
gtc ttg act gtc cag ctc ttt gca ttc tta aac cca ctg cct gta gaa      155
Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val Glu
5                   10                  15                  20
gca gac att tta gca tat aac ttt gaa aat gca tct cag aca ttt gat      203
Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp
                25                  30                  35
gac ctc cct gca aga ttt ggt tat aga ctt cca gct gaa ggt tta aag      251
Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu Lys
            40                  45                  50
ggt ttt tta att aac tca aaa cca gag aat gcc tgt gaa ccc ata gtg      299
Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile Val
        55                  60                  65
cct cca cca gta aaa gac aat tca tct ggc act ttc atc gtg tta att      347
Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu Ile
    70                  75                  80
aga aga ctt gat tgt aat ttt gat ata aag gtt tta aat gca cag aga      395
Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln Arg
85                  90                  95                  100
gca gga tac aag gca gcc ata gtt cac aat gtt gat tct gat gac ctc      443
Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp Leu
                105                 110                 115
att agc atg gga tcc aac gac att gag gta cta aag aaa att gac att      491
Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp Ile
            120                 125                 130
cca tct gtc ttt att ggt gaa tca tca gct agt tct ctg aaa gat gaa      539
Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp Glu
        135                 140                 145
ttc aca tat gaa aaa ggg ggc cac ctt atc tta gtt cca gaa ttt agt      587
Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe Ser
    150                 155                 160
ctt cct ttg gaa tac tac cta att ccc ttc ctt atc ata gtg ggc atc      635
Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly Ile
165                 170                 175                 180
tgt ctc atc ttg ata gtc att ttc atg atc aca aaa ttt gtc cag gat      683
Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln Asp
                185                 190                 195
aga cat aga gct aga aga aac aga ctt cgt aaa gat caa ctt aag aaa      731
Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys Lys
            200                 205                 210
ctt cct gta cat aaa ttc aag aaa gga gat gag tat gat gta tgt gcc      779
Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys Ala
        215                 220                 225
att tgt ttg gat gag tat gaa gat gga gac aaa ctc aga atc ctt ccc      827
Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu Pro
    230                 235                 240
tgt tcc cat gct tat cat tgc aag tgt gta gac cct tgg cta act aaa      875
Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr Lys
245                 250                 255                 260
acc aaa aaa acc tgt cca gtg tgc agg caa aaa gtt gtt cct tct caa      923
Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser Gln
                265                 270                 275
ggc gat tca gac tct gac aca gac agt agt caa gaa gaa aat gaa gtg      971
Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu Val
            280                 285                 290
aca gaa cat acc cct tta ctg aga cct tta gct tct gtc agt gcc cag     1019
Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala Gln
        295                 300                 305
tca ttt ggg gct tta tcg gaa tcc cgc tca cat cag aac atg aca gaa     1067
```

```
Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr Glu
    310                 315                 320
tct tca gac tat gag gaa gac gac aat gaa gat act gac agt agt gat     1115
Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp
325                 330                 335                 340
gca gaa aat gaa att aat gaa cat gat gtc gtg gtc cag ttg cag cct     1163
Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln Pro
                345                 350                 355
aat ggt gaa cgg gat tac aac ata gca aat act gtt tgactttcag          1209
Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
            360                 365
aagatgattg gtttatttcc ctttaaaatg attaggtata tactgtaatt tgatttttg    1269
ctcccttaaa agatttctgt agaaataact tatttttag tactctacag tttaatcaaa    1329
ttactgaaac aggacttttg atctggtatt tatctgccaa gaatatactt cattcactaa    1389
taatagactg gtgctgtaac tcaagcatca attcagctct tcttttggaa tgaaagtata    1449
gccaaaacaa aaaaaaaaaa a                                             1470

<210> 154
<211> 982
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 72..197
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIT/FP
<220>
<221> polyA_site
<222> 970..982
<400> 154
gctgcctgtt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc     60
tcaagaatga g atg gat tct agg gtg tct tca cct gag aag caa gat aaa      110
             Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys
                -40                 -35                 -30
gag aat ttc gtg ggt gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg      158
Glu Asn Phe Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp
            -25                 -20                 -15
atc ctg ttt tcc ctc tct ttc ctg ttg gtg atc att acc ttc ccc atc      206
Ile Leu Phe Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile
        -10                 -5                  1
tcc ata tgg atg tgc ttg aag atc att agg gag tat gaa cgt gct gtt      254
Ser Ile Trp Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val
    5                   10                  15
gta ttc cgt ctg gga cgc atc caa gct gac aaa gcc aag ggg cca ggt      302
Val Phe Arg Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly
20                  25                  30                  35
ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aag gtt gac ctc      350
Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu
                40                  45                  50
cga aca gtt act tgc aac att cct cca caa gag atc ctc acc aga gac      398
Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp
            55                  60                  65
tcc gta act act cag gta gat gga gtt gtc tat tac aga atc tat agt      446
Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser
        70                  75                  80
gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa gca aca ttt      494
Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe
```

```
    85                  90                  95
ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca cag acc ttg      542
Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu
100                 105                 110                 115
tcc cag atc tta gct gga cga gaa gag atc gcc cat agc atc cag act      590
Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr
                120                 125                 130
tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg      638
Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val
            135                 140                 145
gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga tcc atg gca      686
Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala
        150                 155                 160
gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc ctt gca gct      734
Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala
    165                 170                 175
gaa gga gaa atg agt gct tcc aaa tcc ctg aag tca gcc tcc atg gtg      782
Glu Gly Glu Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val
180                 185                 190                 195
ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg cag acc ttg      830
Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu
                200                 205                 210
agc acg gta gcc acc gag aag aat tct acg att gtg ttt cct ctg ccc      878
Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro
            215                 220                 225
atg aat ata cta gag ggc att ggt ggc gtc agc tat gat aac cac aag      926
Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys
        230                 235                 240
aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaa    982
Lys Leu Pro Asn Lys Ala
    245

<210> 155
<211> 455
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 425..430
<220>
<221> polyA_site
<222> 443..455
<400> 155
gtt atg cca ccc aga aac cta ctg gag tta ctt att aac atc aag gct       48
    Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala
    1               5                   10                  15
gga acc tat ttg cct cag tcc tat ctg att cat gag cac atg gtt att       96
Gly Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile
                20                  25                  30
act gat cgc atc gaa aac att gat cac ctg ggt ttc ttt att tat cga      144
Thr Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg
            35                  40                  45
ctg tgt cat gac aag gaa act tac aaa ctg caa cgc aga gaa act att      192
Leu Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile
        50                  55                  60
aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat      240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His
    65                  70                  75
```

```
ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca      289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
80                  85                  90
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg  349
cagtgattat tttttaaagt cttctttcat gtaagtagca aacagggctt tactatcttt  409
tcatctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa                 455

<210> 156
<211> 738
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 90..278
<223> Von Heijne matrix
      score 3.5
      seq GLVCAGLADMARP/AE
<220>
<221> polyA_signal
<222> 704..709
<220>
<221> polyA_site
<222> 724..738
<400> 156
gggaaaagtg actagctccc cttcgttgtc agccagggac gagaacacag ccacgctccc   60
acccggctgc caacgatccc tcggcggcg atg tcg gcc gcc ggt gcc cga ggc    113
                              Met Ser Ala Ala Gly Ala Arg Gly
                                                  -60
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg    161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu
-55                  -50                 -45                 -40
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca    209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr
                -35                 -30                 -25
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga    257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly
            -20                 -15                 -10
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct    305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser
        -5                  1                   5
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta    353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val
10                  15                  20                  25
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg    401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly
                30                  35                  40
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa    449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu
            45                  50                  55
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct       500
Leu Lys Ala Lys Ala His Lys
        60
agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaagcta  560
actgtgtgtt tagaaggcac tgtaactggt agctagttct tgattcaata gaaaaatgca  620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta  680
acatttttct accatttgtc cgtaataaac catacttgct cgtaaaaaaa aaaaaaaa    738

<210> 157
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<211> 649
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 88..147
<223> Von Heijne matrix
score 12.3999996185303
seq ALLLGALLGTAWA/RR
<220>
<221> polyA_signal
<222> 619..624
<220>
<221> polyA_site
<222> 637..649
<400> 157

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ccaaagtgag agtccagcgg tcttccagcg cttgggccac ggcggcggcc ctgggagcag      60
aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg     114
                              Met Lys Gly Trp Gly Trp Leu Ala Leu
                              -20                 -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat       162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
    -10                 -5                  1                   5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa       210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
                10                  15                  20
att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg       258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
            25                  30                  35
atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt       306
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
        40                  45                  50
ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa     359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
    55                  60
aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct     419
catttggaag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa     479
tactttgttt ctgctgtaga atttgttagc aaacagggag tcctgatcag cacccttctc     539
cacatccaca tgactggttt ttaatgtagc actgtggtat acatgcaaac atccgttcaa     599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa                649
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<210> 158
<211> 714
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 33..92
<223> Von Heijne matrix
score 12.3999996185303
seq ALLLGALLGTAWA/RR
<220>
<221> polyA_site
<222> 703..714
<400> 158

```
agcagaggtg gagcgacccc attacgctaa ag atg aaa ggc tgg ggt tgg ctg        53
                                     Met Lys Gly Trp Gly Trp Leu
                                     -20                 -15
```

```
gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc      101
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser
            -10                 -5                  1
cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa      149
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu
    5                   10                  15
tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct      197
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser
20                  25                  30                  35
ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat      245
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr
                40                  45                  50
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac      293
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp
            55                  60                  65
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag      341
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys
        70                  75                  80
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac      389
Asn Tyr Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp
    85                  90                  95
cta caa ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt      437
Leu Gln Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe
100                 105                 110                 115
gcg tgt ggg agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc      485
Ala Cys Gly Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe
                120                 125                 130
ttt tcc cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga      533
Phe Ser Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg
            135                 140                 145
aca gat ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta          578
Thr Asp Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu
        150                 155                 160
tgaaccactg gagcagccca cactggcttg atggatcacc cccaggaggg gaaaatggtg    638
gcaatgcctt ttatatatta tgtttttact gaaattaact gaaaaaatat gaaaccaaaa    698
gtacaaaaaa aaaaaa                                                   714

<210> 159
<211> 596
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 33..107
<223> Von Heijne matrix
      score 5
      seq MFAASLLAMCAGA/EV
<220>
<221> polyA_signal
<222> 546..551
<220>
<221> polyA_site
<222> 584..596
<400> 159
cacagttcct ctcctcctag agcctgccga cc atg ccc gcg ggc gtg ccc atg       53
                                    Met Pro Ala Gly Val Pro Met
                                    -25                 -20
tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc gca      101
```

```
Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala
            -15                 -10                 -5
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct      149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro
        1               5                   10
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg      197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu
15                  20                  25                  30
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa      245
Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys
                35                  40                  45
taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt    305
gcatcaaact acttgtcctt aagcacttag tctaatgcta actgcaagag gaggtgctca    365
gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac    425
tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg tttagtcttg    485
aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt atttcatata    545
aattaagaaa ttatttaaaa ctatgaacta gtttcattaa aaaaaaaaga a              596

<210> 160
<211> 403
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 375..380
<220>
<221> polyA_site
<222> 390..403
<400> 160
tgaagagaat ggctgttgca gtcggcgtca gagcagctcc agtgccgggg attcggacgg     60
agagcgcgag gactcggcgg ctgagcgcgc ccgacagcag ctagaggcgc tgctcaacaa    120
gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt     169
     Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe
     1               5                   10                  15
ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag      217
Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu
                20                  25                  30
ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg      265
Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu
            35                  40                  45
ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag      313
Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln
        50                  55                  60
agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc       363
Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu
    65                  70
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa                         403

<210> 161
<211> 727
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 126..575
<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPPASA/SQ
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<220>
<221> polyA_signal
<222> 670..675
<220>
<221> polyA_site
<222> 721..727
<220>
<221> misc_feature
<222> 257,376..377
<223> n=a, g, c or t
<400> 161
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag 60
gacccggggt agggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg 120
gtcgg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag 170
Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
-150 -145 -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg 218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-135 -130 -125 -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag 266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
-115 -110 -105
ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga 314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
-100 -95 -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc 362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
-85 -80 -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc 410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
-70 -65 -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac 458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
-55 -50 -45 -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag 506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
-35 -30 -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca 554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
-20 -15 -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg 602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
-5 1 5
agc cac cgt gcc cgg cag aga aaa act gct taaggttgaa aagagaaatt 652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10 15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga 712
agcaaaaaaa aaaaa 727

<210> 162
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<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 90..155
<223> Von Heijne matrix
score 5.90000009536743

seq IILGCLALFLLLQ/RK
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<222> 913..918
<220>
<221> polyA_site
<222> 932..944
<400> 162
gaatcaggtt ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt 60
tctgcttctg gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg 113
Met Glu Leu Ile Ser Pro Thr Val
-20 -15
att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag 161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
-10 -5 1
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga 209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
5 10 15
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca 257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala
20 25 30
aga atc aag gta tgt ggt cgt ggc aga cgg ggt ctc cag agg aga caa 305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln
35 40 45 50
tgc ttt ctt ttt taaactttct ttcattgact cttaagtgca gggctagaac 357
Cys Phe Leu Phe
acggggaaca tacctgcttg cctcaactaa aggatctagt catttctgaa ttcctctact 417
aacaattaac aacaatatcc tgtgcaaaat tttgcgaaag aaatgaaata caattgcagc 477
gtgcatcgac atttttggaa gtagagatta acttttcgta tttttacttc atcgaagtta 537
agttccaaat gtgtatgtgt taagtaaatg ttttcagtaa ttgggaaaga taaagtgtaa 597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta 657
ttgtacaaat tgcttgcaca gttggtccgt acacaataga caggctctgt atttttagct 717
gacgttgtta tttgatgatg atgtactcca ttttcactac ggcccgaaga gactagtaat 777
cctccttgta gtagatgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag 837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat 897
ggtatttgat tgtctaataa atttgtatga tattaaaaaa aaaaaaa 944

<210> 163
<211> 598
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<213> Homo sapiens
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<223> Von Heijne matrix
score 3.90000009536743
seq LETCGLLVSLVES/IW
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<221> polyA_signal
<222> 561..566
<220>
<221> polyA_site
<222> 587..598
<400> 163
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag 60
gacccggggt agggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg 120
gtcgg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag 170
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys

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                      -50                 -45                 -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
                  -35                 -30                 -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      266
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
              -20                 -15                 -10
ctg gtt tca cta gtg gaa agc att tgg ctg cat ata aca gaa aac cag      314
Leu Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln
         -5                  1                   5
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      362
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
10                  15                  20                  25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag      410
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
                  30                  35                  40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctgattg    470
tcctcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc    530
ccccatgttc aatccatcct cccaccttgg aataaatgct ttcttttcac aatgagaaaa    590
aaaaaaaa                                                            598

<210> 164
<211> 360
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<213> Homo sapiens
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<222> 85..150
<223> Von Heijne matrix
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<221> polyA_site
<222> 349..360
<400> 164
caggttccgt agccacagaa aagaagcaag ggacggcagg actgtttcac acttttctgc     60
ttctggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att       111
                         Met Glu Leu Ile Ser Pro Thr Val Ile
                                    -20                 -15
ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat      159
Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn
              -10                 -5                  1
ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt      207
Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val
     5                  10                  15
gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga      255
Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg
20                  25                  30                  35
atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg      303
Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met
                  40                  45                  50
acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc          348
Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser
              55                  60                  65
aaaaaaaaaa aa                                                       360

<210> 165
<211> 490
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<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 77..124
<223> Von Heijne matrix
score 4.80000019073486
seq SLFIYIFLTCSNT/SP
<220>
<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 477..490
<400> 165
atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag 60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca 112
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
-15 -10 -5
tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt 160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
1 5 10
ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc 208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
15 20 25
tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc 256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
30 35 40
ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc 304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
45 50 55 60
tgg gac tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact 353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
65 70
gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct 413
cccttgccct ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa 473
gtgaaaaaaa aaaaaaa 490

<210> 166
<211> 488
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 458..463
<220>
<221> polyA_site
<222> 475..488
<400> 166
ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac 55
Met Lys Val Asp Lys Asp
1 5
cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag 103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
10 15 20
gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac 151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr
25 30 35

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agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt      199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys
    40                  45                  50
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg      247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met
55                  60                  65                  70
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag      295
Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys
                75                  80                  85
gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa      343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln
            90                  95                  100
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga        394
Glu Lys Leu Ser Phe Phe Arg
        105
tgtctgagtc ctcaaggtga ctggggactt ggaaccccta ggacctgaac aaccaagact    454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa                               488

<210> 167
<211> 771
<212> DNA
<213> Homo sapiens
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<222> 48..356
<223> Von Heijne matrix
      score 4.90000009536743
      seq VYAFLGLTAPSGS/KE
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<221> polyA_signal
<222> 742..747
<220>
<221> polyA_site
<222> 760..771
<400> 167
ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc       56
                                                Met Val Ile
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa      104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys
-100                -95                 -90                 -85
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa      152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu
                -80                 -75                 -70
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa      200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu
            -65                 -60                 -55
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct      248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro
        -50                 -45                 -40
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt      296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe
    -35                 -30                 -25
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc      344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala
-20                 -15                 -10                 -5
cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca          389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala
                1               5                   10
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tgaaccttga gcactgtgct ttaagcatcc tgaaaaatga gtctccattg cttttataaa    449
atagcagaat tagctttgct tcaaaagaaa taggcttaat gttgaaataa tagattagtt    509
gggttttcac atgcaaacac tcaaaatgaa tacaaaatta aaatttgaac attatggtga    569
ttatggtgag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa    629
atagtgttgt tacctgccaa gccatcctgt atacaccaat gattttacaa agaaaacacc    689
cttccctcct tctgccatta ctatggcaac ctaagtgtat ctgcagctct acattaaaaa    749
ggagaaagag aaaaaaaaaa aa                                             771

<210> 168
<211> 959
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 69..359
<223> Von Heijne matrix
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<221> polyA_signal
<222> 927..932
<220>
<221> polyA_site
<222> 947..959
<400> 168
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ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca     110
         Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro
                -95                 -90                 -85
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta     158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val
            -80                 -75                 -70
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga     206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg
        -65                 -60                 -55
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa     254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys
    -50                 -45                 -40
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac     302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr
-35                 -30                 -25                 -20
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc     350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala
                -15                 -10                 -5
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt     398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu
            1               5                   10
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct             440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
    15                  20                  25
taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc    500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg ccccttttc     560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt    620
ttctggtgta gggtctttct tatttagtga gatctaggga taccacagaa atggttcagt    680
ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga ttctattcag    740
tggatcagaa tcaaactggt acattgatcc acttgagccg ttaagtgctg ccaattgtac    800
aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa taaggacata    860
tttttcttca gattatgttt tatttctttg cattgagtga ggaacataaa atggcttggt    920
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aaaagtaata aaatcagtac aatcactaaa aaaaaaaaa                              959

<210> 169
<211> 464
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 33..98
<223> Von Heijne matrix
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      seq LVVFCLALQLVPG/SP
<220>
<221> polyA_signal
<222> 437..442
<220>
<221> polyA_site
<222> 455..464
<400> 169
gccagaactt actcacccat cccactgaca cc atg aag cct gtg ctg cct ctc        53
                                    Met Lys Pro Val Leu Pro Leu
                                                -20
cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt       101
Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser
-15                 -10                 -5                  1
ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata       149
Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile
            5                   10                  15
tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc       197
Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys
        20                  25                  30
gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca       245
Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser
    35                  40                  45
tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa       293
Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu
50                  55                  60                  65
gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc              341
Val Ile Met Pro Ala Asn
                70
tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc     401
caatatctaa cctgcaaatc gtttttgagt ttggcaataa aggctaatct accaaaaaaa     461
aaa                                                                   464

<210> 170
<211> 799
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 110..235
<223> Von Heijne matrix
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      seq LLFDLVCHEFCQS/DD
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<221> polyA_signal
<222> 764..769
<220>
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<221> polyA_site
<222> 787..799
<400> 170
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agctgccaaa caagtacgtt ctgaaaatcc agaatggctt gatgtttac atg cac att 118
Met His Ile
-40
tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat 166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His
-35 -30 -25
tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc 214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val
-20 -15 -10
tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa 262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu
-5 1 5
cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat 310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr
10 15 20 25
gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt 358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu
30 35 40
cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt 406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys
45 50 55
cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa 454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys
60 65 70
agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat 502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp
75 80 85
att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag 550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu
90 95 100 105
acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt 598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys
110 115 120
tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa 646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu
125 130 135
gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac 694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp
140 145 150
ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga 740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
155 160 165
attggaatta cttctgtaca agaaataaac tttatttttc tcactgaaaa aaaaaaaaa 799

<210> 171
<211> 320
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_site
<222> 308..320
<400> 171
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Met Pro His Ser Lys Pro

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                                                1               5
ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt      103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
            10                  15                  20
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta      151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
        25                  30                  35
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc      199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
    40                  45                  50
ggt gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggt      254
Gly Val Phe Asn Leu
55
tgttgtgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa    314
aaaaaa                                                              320

<210> 172
<211> 331
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 129..209
<223> Von Heijne matrix
      score 4.90000009536743
      seq CLLSYIALGAIHA/KI
<220>
<221> polyA_site
<222> 318..331
<400> 172
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cacctctagc ctgctcattt ccagctcaga aattctacta atggcgtttt ttcttcctga    120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc      170
         Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
                -25                 -20                 -15
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt      218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
            -10                 -5                  1
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg      266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
    5                   10                  15
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc       316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
20                  25
caaaaaaaaa aaaaa                                                    331

<210> 173
<211> 1075
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 78..359
<223> Von Heijne matrix
      score 4.19999980926514
      seq IILTAVYFALSIS/LH
<220>
<221> polyA_signal
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<222> 1042..1047
<220>
<221> polyA_site
<222> 1063..1075
<400> 173
gtggtaggga gcagccagga gcggttttct gggaactgtg ggatgtgccc ttgggggccc 60
gagaaaacag aaggaag atg ctc cag acc agt aac tac agc ctg gtg ctc 110
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu
-90 -85
tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc 158
Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe
-80 -75 -70
tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc 206
Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile
-65 -60 -55
atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg 254
Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met
-50 -45 -40
ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc 302
Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe
-35 -30 -25 -20
cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc 350
His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu
-15 -10 -5
agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc 398
Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser
1 5 10
aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag 446
Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln
15 20 25
aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta 494
Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val
30 35 40 45
aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag 542
Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys
50 55 60
gag ttc atg caa gtt cga agg tgacctcttg tcacactgat ggatactttt 593
Glu Phe Met Gln Val Arg Arg
65
ccttcctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcatgggca 653
aacagctgga ctttccaagg aaggttcaga ctagctgtgt tcagcattca agaaggaaga 713
tcccccctct tgcacaatta gagtgtcccc atcggtctcc agtgcggcat cccttccttg 773
ccttctacct ctgttccacc cccttccttc ctctcctctc tgtaccattc attctccctg 833
accggccttt cttgccgagg gttctgtggc tcttaccctt gtgaagcttt tcctttagcc 893
tgggacagaa ggacctcccg gcccccaaag gatctcccag tgaccaaagg atgcgaagag 953
tgatagttac gtgctcctga ctgatcacac cgcagacatt tagattttta tacccaaggc 1013
actttaaaaa aatgttttat aaatagagaa taaattgaat tcttgttcca aaaaaaaaaa 1073
aa 1075

<210> 174
<211> 632
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 62..265
<223> Von Heijne matrix
score 4.59999990463257

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      seq LPFSLVSMLVTQG/LV
<220>
<221> polyA_signal
<222> 602..607
<220>
<221> polyA_site
<222> 621..632
<400> 174
cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcat     60
c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt    109
  Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
             -65                 -60                 -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
         -50                 -45                 -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
    -35                 -30                 -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20                 -15                 -10                 -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
                1                   5                  10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
        15                  20                  25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
    30                  35                  40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg      445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
45                  50                  55                  60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt      493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
                65                  70                  75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact        543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
            80                  85
ttcgaagttt tttaaacctc tgaatttgta cacatttaaa atttcaagtg tactttaaaa    603
taaaatactt ctaatgtaaa aaaaaaaaa                                     632

<210> 175
<211> 430
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 402..407
<220>
<221> polyA_site
<222> 419..430
<400> 175
gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca     53
                         Met Lys Val Glu Glu Glu His Thr Asn Ala
                         1               5                   10
ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata      101
Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile
```

```
                15                  20                  25
tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt      149
Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser
            30                  35                  40
gtc gat atg aac ata acg tac atg tca cct gca aaa tta gga gag gat      197
Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp
        45                  50                  55
ata gtg att aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt      245
Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe
    60                  65                  70
acc tct gtg ggt ctg acc aac aag gcc aca gga aaa tta ata gca caa      293
Thr Ser Val Gly Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln
75                  80                  85                  90
gga aga cac aca aaa cac ctg gga aac tgagagaaca gcagaatgac            340
Gly Arg His Thr Lys His Leu Gly Asn
                95
ctaaagaaac ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg    400
aaataaacta gcaaaaccaa aaaaaaaaaa                                    430

<210> 176
<211> 185
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 42..113
<223> Von Heijne matrix
      score 3.70000004768372
      seq ILFNLLIFLCGFT/NY
<220>
<221> polyA_site
<222> 172..185
<400> 176
ctttcagaac tcactgccaa gagccctgaa caggagccac c atg cag tgc ttc agc     56
                                                Met Gln Cys Phe Ser
                                                            -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      104
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
                -15                 -10                 -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      152
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
            1               5                   10
cat aaa cct gtt aca atg taaaaaaaaa aaaaa                            185
His Lys Pro Val Thr Met
    15

<210> 177
<211> 585
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 108..170
<223> Von Heijne matrix
      score 5.5
      seq SFLPSALVIWTSA/AF
<220>
<221> polyA_signal
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<222> 550..555
<220>
<221> polyA_site
<222> 574..585
<400> 177
cacgttcctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc 60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg 116
Met Trp Trp
-20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca 164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
-15 -10 -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat 212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
1 5 10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca 260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15 20 25 30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt 308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
35 40 45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaaa 364
Gln Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt 424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg 484
gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaa 544
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa a 585

<210> 178
<211> 613
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 118..171
<223> Von Heijne matrix
score 5.90000009536743
seq ALALLWSLPASDL/GR
<220>
<221> polyA_signal
<222> 583..588
<220>
<221> polyA_site
<222> 602..613
<400> 178
ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg 60
gagctgccgc acagagcctg gtgtccacaa gcttccaggt tggggttgga gcctggg 117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct 165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
-15 -10 -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt 213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
1 5 10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc 261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15 20 25 30
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt 309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

```
                35                  40                  45
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca              351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
            50                  55                  60
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg    411
tcgaaaataa gcaccttggt aactaaaccc ctctaatagc tataaaggct ttagttctgt    471
attgattaag ttactgtaaa agcttgggtt tatttttgta ggacttaatg gctaagaatt    531
agaacatagc aaggggggctc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat    591
gcaaaccttt aaaaaaaaaa aa                                             613

<210> 179
<211> 427
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 128..268
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK
<220>
<221> polyA_signal
<222> 410..415
<220>
<221> polyA_site
<222> 424..427
<400> 179
agcttggatt tacactgggc aacgtggttg gaatgtatct ggctcagaac tatgatatac     60
caaacctggc taaaaaactt gaagaaatta aaaaggactt ggatgccaag aagaaacccc    120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct      169
        Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser
                -45                 -40                 -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt      217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe
            -30                 -25                 -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt      265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe
        -15                 -10                 -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca      313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr
    1               5                   10                  15
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg      361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly
                20                  25                  30
agg ttc taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa       417
Arg Phe
aaaaacaaaa                                                          427

<210> 180
<211> 905
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 149..457
<223> Von Heijne matrix
      score 4.90000009536743
      seq FLLAQTTLRNVLG/TQ
```

<220>
<221> polyA_site
<222> 893..912
<400> 180
gctgcctgtt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc 60
tcaagaatga gatggattct agggtgtctt cacctgagaa gcaagataaa gagaatttcg 120
tgggtgtcaa caataaacgg cttggtgt atg tgg ctg gat cct gtt ttc cct 172
Met Trp Leu Asp Pro Val Phe Pro
-100
ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg 220
Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
-95 -90 -85 -80
ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa 268
Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
-75 -70 -65
gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc 316
Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
-60 -55 -50
acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga 364
Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
-45 -40 -35
atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa 412
Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln
-30 -25 -20
gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca 460
Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
-15 -10 -5 1
cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc 508
Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
5 10 15
atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg 556
Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
20 25 30
gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga 604
Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
35 40 45
tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc 652
Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
50 55 60 65
ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc 700
Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
70 75 80
tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg 748
Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
85 90 95
cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt 796
Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
100 105 110
cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat 844
Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp
115 120 125
aac cac aag aag ctt cca aat aaa gcc tgaggtcctc ttgcggtagt 891
Asn His Lys Lys Leu Pro Asn Lys Ala
130 135
caaaaaaaaa aaaa 905

<210> 181
<211> 307

<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -13..-1
<400> 181

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Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
            -10                 -5                  1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
    5                   10                  15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20                  25                  30                  35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
                40                  45                  50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
            55                  60                  65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
        70                  75                  80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
    85                  90                  95
Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Tyr Lys Gly Leu
100                 105                 110                 115
Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Leu Ser Ser
                120                 125                 130
Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr
            135                 140                 145
Val Thr Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys
        150                 155                 160
Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp
    165                 170                 175
Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu
180                 185                 190                 195
Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu
                200                 205                 210
Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val
            215                 220                 225
Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn
        230                 235                 240
Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Ser Gly Gly Tyr
    245                 250                 255
Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu
260                 265                 270                 275
Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Val
                280                 285                 290
Lys Lys Lys
```

<210> 182
<211> 59
<212> PRT
<213> Homo sapiens
<400> 182

```
Met Met Tyr Val Ser Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu
1               5                   10                  15
Phe Asp Tyr Val Val Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu
            20                  25                  30
Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys
        35                  40                  45
Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile
```

50 55

<210> 183
<211> 97
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -28..-1
<400> 183

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Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
            -25                 -20                 -15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
        -10                 -5                  1
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
5                   10                  15                  20
His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro
                25                  30                  35
Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu
            40                  45                  50
Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val
        55                  60                  65
Ala
```

<210> 184
<211> 52
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1
<400> 184

```
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
        -30                 -25                 -20
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
    -15                 -10                 -5
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
1                   5                   10                  15
Thr Phe Ala His
            20
```

<210> 185
<211> 124
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -97..-1
<400> 185

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Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
        -95                 -90                 -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
    -80                 -75                 -70
Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
-65                  -60                 -55                 -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
                -45                 -40                 -35
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
```

```
            -30                 -25                 -20
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
        -15                 -10                 -5
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
    1               5                   10                  15
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
                20                  25
```

<210> 186
<211> 230
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -24..-1
<400> 186

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Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
                -20                 -15                 -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
            -5                  1                   5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
    10                  15                  20
Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
25                  30                  35                  40
Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
                45                  50                  55
Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
            60                  65                  70
Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
        75                  80                  85
Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly
    90                  95                  100
Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu
105                 110                 115                 120
Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile
                125                 130                 135
Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile
            140                 145                 150
Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser
        155                 160                 165
Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser
    170                 175                 180
Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr
185                 190                 195                 200
Ser Leu Thr Gly Tyr Val
                205
```

<210> 187
<211> 72
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1
<400> 187

```
Met Phe Ala Leu Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
        -30                 -25                 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Ala Gly Gly Ser Phe Gly
```

```
    -15                 -10                 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1               5                   10                  15
Asp Pro Glu Leu Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu
            20                  25                  30
Ser Glu Tyr Glu Gly Ser Ile Cys
        35                  40
```

<210> 188
<211> 88
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -33..-1
<400> 188

```
Met Ser Gln Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly
            -30                 -25                 -20
Pro Phe Ser Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr
        -15                 -10                 -5
Ser Leu Phe Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly
    1               5                   10                  15
Leu Ile Leu Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe
            20                  25                  30
Ala Leu Ser Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met
            35                  40                  45
Asp Pro Lys Arg Lys Thr Lys Cys
        50                  55
```

<210> 189
<211> 106
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -32..-1
<400> 189

```
Met Phe Ala Pro Ala Val Thr Arg Ala Phe Arg Lys Asn Lys Thr Leu
        -30                 -25                 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
    -15                 -10                 -5
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1               5                   10                  15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
            20                  25                  30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
        35                  40                  45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg
    50                  55                  60
Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
65                  70
```

<210> 190
<211> 267
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL

<222> -21..-1
<400> 190
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
15 20 25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
30 35 40
Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr Lys Gln Val His Ala
45 50 55
Leu Ser Pro Glu Glu Asn Val Ile Ile Lys Leu Asn Lys Ala Gly Leu
60 65 70 75
Val Leu Gly Ile Leu Ser Cys Leu Gly Leu Ser Ile Val Ala Asn Phe
80 85 90
Gln Lys Thr Thr Leu Phe Ala Ala His Val Ser Gly Ala Val Leu Thr
95 100 105
Phe Gly Met Gly Ser Leu Tyr Met Phe Val Gln Thr Ile Leu Ser Tyr
110 115 120
Gln Met Gln Pro Lys Ile His Gly Lys Gln Val Phe Trp Ile Arg Leu
125 130 135
Leu Leu Val Ile Trp Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys
140 145 150 155
Ser Ser Val Leu His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys
160 165 170
Leu His Trp Asn Pro Glu Asp Lys Gly Tyr Ala Leu His Met Ile Thr
175 180 185
Thr Ala Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu
190 195 200
Thr Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
205 210 215
Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn Asn
220 225 230 235
Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile Arg
240 245

<210> 191
<211> 108
<212> PRT
<213> Homo sapiens
<400> 191
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile
1 5 10 15
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu
20 25 30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg
35 40 45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu
50 55 60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg
65 70 75 80
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
85 90 95
Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr
100 105

<210> 192

<211> 69
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -46..-1
<400> 192
Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile
-45 -40 -35
Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys
-30 -25 -20 -15
Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu
-10 -5 1
Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu
5 10 15
Lys Tyr His Trp Pro
20

<210> 193
<211> 251
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -28..-1
<400> 193
Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
-25 -20 -15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
-10 -5 1
Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
5 10 15 20
Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys Val Arg Arg
25 30 35
Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr
40 45 50
Glu Phe Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr
55 60 65
Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile Asn Arg Ser
70 75 80
Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe
85 90 95 100
Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys
105 110 115
Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Leu Val
120 125 130
Val Glu Met Gly Gly Arg Cys Glu Phe Glu Glu Val Gln Gly Phe Leu
135 140 145
Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg
150 155 160
Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn
165 170 175 180
Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Asn Met Leu
185 190 195
Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys
200 205 210
Tyr Trp Gly Lys Phe Tyr Met Pro Lys Arg Val
215 220

<210> 194
<211> 99
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -48..-1
<400> 194

```
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
            -45                 -40                 -35
Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
        -30                 -25                 -20
Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
    -15                 -10                 -5
Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
1                   5                   10                  15
Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
            20                  25                  30
Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
        35                  40                  45
Glu Val Leu
    50
```

<210> 195
<211> 81
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -31..-1
<400> 195

```
Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro
    -30                 -25                 -20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro
-15                 -10                 -5                  1
Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser
            5                   10                  15
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser
        20                  25                  30
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp
    35                  40                  45
Leu
50
```

<210> 196
<211> 150
<212> PRT
<213> Homo sapiens
<400> 196

```
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu Leu Thr
1               5                   10                  15
Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp His Gly
            20                  25                  30
Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu Glu Pro
        35                  40                  45
Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr Tyr Ile
    50                  55                  60
```

```
Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser Phe Phe
65                  70                  75                  80
Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg Lys Val
                85                  90                  95
Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser His Leu
            100                 105                 110
Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser His Asn His
        115                 120                 125
Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr Val Thr Ser
    130                 135                 140
Val Ser Thr Lys Lys Lys
145                 150
```

<210> 197
<211> 273
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -45..-1
<400> 197

```
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
-45                 -40                 -35                 -30
Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
                -25                 -20                 -15
Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
            -10                 -5                  1
Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
    5                   10                  15
Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
20                  25                  30                  35
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
                40                  45                  50
Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
            55                  60                  65
Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
        70                  75                  80
Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
    85                  90                  95
Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
100                 105                 110                 115
Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
                120                 125                 130
Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
            135                 140                 145
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
        150                 155                 160
Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
    165                 170                 175
Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys Gln
180                 185                 190                 195
Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
                200                 205                 210
Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
            215                 220                 225
Leu
```

<210> 198

<211> 413
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -37..-1
<400> 198
Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro
-35 -30 -25
Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His
-20 -15 -10
Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr
-5 1 5 10
Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser
15 20 25
Phe Glu His Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg
30 35 40
Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu
45 50 55
Cys Asp His His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg
60 65 70 75
Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His
80 85 90
His Thr Val Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu
95 100 105
Gln Ala Val Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys
110 115 120
Leu Glu Ala Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val
125 130 135
Gln Thr Glu Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser
140 145 150 155
Ile Leu Asn Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu
160 165 170
Glu Lys Lys Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val
175 180 185
Gln Gln Lys Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg
190 195 200
Ser Gln Trp Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met
205 210 215
Lys Trp Ser Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys
220 225 230 235
Lys Leu Lys Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln
240 245 250
Met Phe Arg Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr
255 260 265
Leu Asn Ser Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln
270 275 280
Arg Gln Val Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr
285 290 295
Gly Val Leu Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu
300 305 310 315
Val Asp Val Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg
320 325 330
Thr Tyr Ser Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg
335 340 345
Gln Asn Leu Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile
350 355 360
Gly Leu Gln Asn Lys Cys Lys Tyr Gly Ala Lys Lys Lys

365 370 375

<210> 199
<211> 393
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -19..-1
<400> 199

```
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
                -15                 -10                 -5
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
            1                   5                  10
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
    15                  20                  25
Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
30                  35                  40                  45
Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
                50                  55                  60
Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
            65                  70                  75
Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
        80                  85                  90
Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
    95                  100                 105
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
110                 115                 120                 125
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
                130                 135                 140
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
            145                 150                 155
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
        160                 165                 170
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
    175                 180                 185
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
190                 195                 200                 205
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
                210                 215                 220
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
            225                 230                 235
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
        240                 245                 250
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys
    255                 260                 265
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met
270                 275                 280                 285
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg
                290                 295                 300
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser
            305                 310                 315
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg
        320                 325                 330
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu
    335                 340                 345
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln
350                 355                 360                 365
```

Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
370

<210> 200
<211> 381
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -13..-1
<400> 200

```
Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
            -10                 -5                  1
Thr Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val
    5                   10                  15
Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
20                  25                  30                  35
Asp Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
                40                  45                  50
Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
            55                  60                  65
Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
        70                  75                  80
Ile Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
    85                  90                  95
Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp
100                 105                 110                 115
Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp
                120                 125                 130
Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp
            135                 140                 145
Glu Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe
        150                 155                 160
Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly
    165                 170                 175
Ile Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln
180                 185                 190                 195
Asp Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys
                200                 205                 210
Lys Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys
            215                 220                 225
Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu
        230                 235                 240
Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr
    245                 250                 255
Lys Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser
260                 265                 270                 275
Gln Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu
                280                 285                 290
Val Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala
            295                 300                 305
Gln Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr
        310                 315                 320
Glu Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser
    325                 330                 335
Asp Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln
340                 345                 350                 355
Pro Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
```

360 365

<210> 201
<211> 291
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 201

```
Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
        -40                 -35                 -30
Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
    -25                 -20                 -15
Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
-10                 -5                  1                   5
Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val Val Phe Arg
            10                  15                  20
Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu
        25                  30                  35
Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val
    40                  45                  50
Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr
55                  60                  65                  70
Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser
                75                  80                  85
Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala
            90                  95                  100
Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile
        105                 110                 115
Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp
    120                 125                 130
Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys
135                 140                 145                 150
Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
                155                 160                 165
Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
            170                 175                 180
Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
        185                 190                 195
Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
    200                 205                 210
Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
215                 220                 225                 230
Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
                235                 240                 245
Asn Lys Ala
```

<210> 202
<211> 92
<212> PRT
<213> Homo sapiens
<400> 202

```
Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly
1               5                   10                  15
Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr
            20                  25                  30
Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu
```

```
        35                  40                  45
Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys
    50                  55                  60
Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe
65                  70                  75                  80
Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
                85                  90
```

<210> 203
<211> 127
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -63..-1
<400> 203

```
Met Ser Ala Ala Gly Ala Arg Gly Leu Arg Ala Thr Tyr His Arg Leu
            -60                 -55                 -50
Pro Asp Lys Val Glu Leu Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr
        -45                 -40                 -35
Asn His Pro Ala Gly Pro Arg Thr Val Phe Phe Trp Ala Pro Ile Met
    -30                 -25                 -20
Lys Trp Gly Leu Val Cys Ala Gly Leu Ala Asp Met Ala Arg Pro Ala
-15                 -10                 -5                  1
Glu Lys Leu Ser Thr Ala Gln Ser Ala Val Leu Met Ala Thr Gly Phe
            5                   10                  15
Ile Trp Ser Arg Tyr Ser Leu Val Ile Ile Pro Lys Asn Trp Ser Leu
        20                  25                  30
Phe Ala Val Asn Phe Phe Val Gly Ala Ala Gly Ala Ser Gln Leu Phe
    35                  40                  45
Arg Ile Trp Arg Tyr Asn Gln Glu Leu Lys Ala Lys Ala His Lys
50                  55                  60
```

<210> 204
<211> 84
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -20..-1
<400> 204

```
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20                 -15                 -10                 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
                1                   5                   10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
            15                  20                  25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
        30                  35                  40
Ser Val Val Glu Val Thr Val Thr Val Pro Pro Asn Lys Val Ala His
45                  50                  55                  60
Ser Gly Phe Gly
```

<210> 205
<211> 182
<212> PRT
<213> Homo sapiens
<220>

<221> SIGNAL
<222> -20..-1
<400> 205

```
Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
-20                 -15                 -10                 -5
Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
                  1                   5                  10
Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
         15                  20                  25
Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
     30                  35                  40
Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
45                  50                  55                  60
Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
                  65                  70                  75
Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
             80                  85                  90
Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
         95                 100                 105
Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
    110                 115                 120
Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
125                 130                 135                 140
Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
                 145                 150                 155
Ile Ser His Asp Glu Leu
             160
```

<210> 206
<211> 71
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -25..-1
<400> 206

```
Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
-25                 -20                 -15                 -10
Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
                 -5                   1                   5
Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
         10                  15                  20
Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
     25                  30                  35
Ser Gln Gln Glu Glu Leu Lys
40                  45
```

<210> 207
<211> 73
<212> PRT
<213> Homo sapiens
<400> 207

```
Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu
1                   5                  10                  15
Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu Phe
             20                  25                  30
Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu Gly
         35                  40                  45
```

```
Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln Arg
    50                  55                  60
Glu Ser Leu Thr Gly Pro Pro Tyr Leu
65                  70

<210> 208
<211> 169
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -150..-1
<220>
<221> UNSURE
<222> -67
<223> Xaa = any one of the twenty amino acids
<400> 208
Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys Asp
-150                 -145                 -140                 -135
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
                -130                 -125                 -120
Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu Leu
            -115                 -110                 -105
Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly
        -100                 -95                  -90
Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly Trp
    -85                  -80                  -75
Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro Glu
-70                  -65                  -60                  -55
Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg
                -50                  -45                  -40
Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu Thr
            -35                  -30                  -25
Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Cys
        -20                  -15                  -10
Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val Ser
    -5                   1                    5                   10
His Arg Ala Arg Gln Arg Lys Thr Ala
                15

<210> 209
<211> 76
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 209
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
        -20                  -15                  -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
    -5                   1                    5                   10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
                15                   20                   25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Val Cys Gly Arg Gly
            30                   35                   40
Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
        45                   50
```

<210> 210
<211> 95
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -54..-1
<400> 210

```
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
                -50                 -45                 -40
Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
            -35                 -30                 -25
Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
        -20                 -15                 -10
Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
    -5                  1                   5                   10
Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
                15                  20                  25
Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
            30                  35                  40
```

<210> 211
<211> 92
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 211

```
Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
        -20                 -15                 -10
Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
    -5                  1                   5                   10
Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
                15                  20                  25
Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
            30                  35                  40
Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
        45                  50                  55
Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys
    60                  65                  70
```

<210> 212
<211> 89
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -16..-1
<400> 212

```
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
    -15                 -10                 -5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1                   5                   10                  15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
            20                  25                  30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
```

```
        35                  40                  45
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
    50                  55                  60
Glu Ala Gly Ala Ser Leu Tyr Ser Pro
65                  70
```

<210> 213
<211> 109
<212> PRT
<213> Homo sapiens

```
<400> 213
Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu Phe
1               5                  10                  15
Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg Gln
            20                  25                  30
Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg
        35                  40                  45
Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys Lys
    50                  55                  60
Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln
65                  70                  75                  80
Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp Leu
                85                  90                  95
Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
            100                 105
```

<210> 214
<211> 114
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -103..-1

```
<400> 214
Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile
            -100                -95                 -90
Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile
        -85                 -80                 -75
Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp
    -70                 -65                 -60
Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro
-55                 -50                 -45                 -40
Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp
                -35                 -30                 -25
Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly
            -20                 -15                 -10
Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln
        -5                  1                   5
Gln Ala
10
```

<210> 215
<211> 124
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -97..-1

<400> 215
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
-95 -90 -85
Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
-80 -75 -70
Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
-65 -60 -55 -50
Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
-45 -40 -35
Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
-30 -25 -20
Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
-15 -10 -5
Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
1 5 10 15
Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
20 25

<210> 216
<211> 93
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -22..-1
<400> 216
Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
-20 -15 -10
Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
-5 1 5 10
Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
15 20 25
Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
30 35 40
Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
45 50 55
Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
60 65 70

<210> 217
<211> 207
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -42..-1
<400> 217
Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
-40 -35 -30
Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
-25 -20 -15
Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
-10 -5 1 5
Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
10 15 20
Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys
25 30 35
Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met

```
    40                  45                  50
Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu
55                  60                  65                  70
Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile
                75                  80                  85
Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu
            90                  95                  100
Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys
        105                 110                 115
Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro
    120                 125                 130
Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu
135                 140                 145                 150
Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr
                155                 160                 165
```

<210> 218
<211> 59
<212> PRT
<213> Homo sapiens
<400> 218

```
Met Pro His Ser Lys Pro Leu Asp Trp Gly Leu Ser Ser Val Ala Glu
1               5                   10                  15
Cys Pro Ala Glu Leu Phe Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly
            20                  25                  30
Pro Gly Leu Asp Ile Leu Arg Cys Val Leu Ser Pro Trp Ala Ser His
        35                  40                  45
Phe Pro Ser Leu Ser Leu Gly Val Phe Asn Leu
    50                  55
```

<210> 219
<211> 56
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -27..-1
<400> 219

```
Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
        -25                 -20                 -15
Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
    -10                 -5                  1                   5
Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val Arg Ala
                10                  15                  20
Trp Cys Ile Gln Pro Trp Ala Lys
            25
```

<210> 220
<211> 162
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -94..-1
<400> 220

```
Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
                -90                 -85                 -80
Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
```

```
            -75                 -70                 -65
Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
        -60                 -55                 -50
Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
    -45                 -40                 -35
Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
-30                 -25                 -20                 -15
Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
                -10                 -5                  1
Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
        5                   10                  15
Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
    20                  25                  30
Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
35                  40                  45                  50
His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
                55                  60                  65
Arg Arg
```

<210> 221
<211> 154
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -68..-1
<400> 221

```
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
            -65                 -60                 -55
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
        -50                 -45                 -40
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
    -35                 -30                 -25
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
-20                 -15                 -10                 -5
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
                1                   5                   10
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
        15                  20                  25
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
    30                  35                  40
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
45                  50                  55                  60
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
                65                  70                  75
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
            80                  85
```

<210> 222
<211> 99
<212> PRT
<213> Homo sapiens
<400> 222

```
Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu His Gly
1               5                   10                  15
Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala Leu Leu
            20                  25                  30
Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn Ile Thr
```

35 40 45
Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His
50 55 60
Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr
65 70 75 80
Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His
85 90 95
Leu Gly Asn

<210> 223
<211> 43
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -24..-1
<400> 223
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-20 -15 -10
Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
-5 1 5
Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
10 15

<210> 224
<211> 69
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -21..-1
<400> 224
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10
Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10
Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
15 20 25
Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
30 35 40
Val Leu Cys Gln Lys
45

<210> 225
<211> 78
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -18..-1
<400> 225
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
-15 -10 -5
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
1 5 10
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr
15 20 25 30
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val

```
                35                  40                  45
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala
            50                  55                  60

<210> 226
<211> 80
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -47..-1
<400> 226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
        -45                 -40                 -35
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
    -30                 -25                 -20
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
-15                 -10                 -5                  1
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
            5                   10                  15
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
        20                  25                  30

<210> 227
<211> 241
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -103..-1
<400> 227
Met Trp Leu Asp Pro Val Phe Pro Leu Phe Pro Val Gly Asp His Tyr
            -100                -95                 -90
Leu Pro His Leu His Met Asp Val Leu Glu Gly Leu Ile Leu Val Leu
        -85                 -80                 -75
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys
    -70                 -65                 -60
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln
-55                 -50                 -45                 -40
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val
                -35                 -30                 -25
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr
            -20                 -15                 -10
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala
        -5                  1                   5
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala
10                  15                  20                  25
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val
                30                  35                  40
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala
            45                  50                  55
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Asn
        60                  65                  70
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro
    75                  80                  85
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr
90                  95                  100                 105
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu
```

```
                110                 115                 120
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys
            125                 130                 135
Ala

<210>  228
<211>  560
<212>  DNA
<213>  Homo sapiens
<220>
<221>  CDS
<222>  (11)..(439)
<220>
<221>  polyA_site
<222>  (547)..(560)
<220>
<221>  polyA_signal
<222>  (530)..(535)
<400>  229
cagaacaatc atg tct gac tcc ctg gtg gtg tgc gag gta gac cca gag        49
           Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu
           1               5                   10
cta aca gaa aag ctg agg aaa ttc cgc ttc cga aaa gag aca gac aat        97
Leu Thr Glu Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn
    15                  20                  25
gca gcc atc ata atg aag gtg gac aaa gac cgg cag atg gtg gtg ctg       145
Ala Ala Ile Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu
30                  35                  40                  45
gag gaa gaa ttt cgg aac att tcc cca gag gag ctc aaa atg gag ttg       193
Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu
                50                  55                  60
ccg gag aga cag ccc agg ttc gtg gtt tac agc tac aag tac gtg cgt       241
Pro Glu Arg Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg
            65                  70                  75
gac gat ggc cga gtg tcc tac cct ttg tgt ttc atc ttc tcc agc cct       289
Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro
        80                  85                  90
gtg ggc tgc aag ccg gaa caa cag atg atg tat gca ggg agt aaa aac       337
Val Gly Cys Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn
    95                  100                 105
agg ctg gtg cag aca gca gag ctc aca aag gtg ttc gaa atc cgc acc       385
Arg Leu Val Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr
110                 115                 120                 125
act gat gac ctc act gag gcc tgg ctc caa gaa aag ttg tct ttc ttt       433
Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe
                130                 135                 140
cgt tga tctctgggct ggggactgaa ttcctgatgt ctgagtcctc aaggtgactg       489
Arg

gggacttgga acccctagga cctgaacaac caagacttta ataaaatttt aaaatgcaaa    549
aaaaaaaaaa a                                                        560

<210>  229
<211>  142
<212>  PRT
<213>  Homo sapiens
<400>  229
```

```
Met Ser Asp Ser Leu Val Val Cys Glu Val Asp Pro Glu Leu Thr Glu
1               5                  10                  15
Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn Ala Ala Ile
            20                  25                  30
Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu Glu Glu Glu
        35                  40                  45
Phe Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu Pro Glu Arg
    50                  55                  60
Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg Asp Asp Gly
65                  70                  75                  80
Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro Val Gly Cys
                85                  90                  95
Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn Arg Leu Val
            100                 105                 110
Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr Thr Asp Asp
        115                 120                 125
Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe Arg
    130                 135                 140
```